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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 308.446 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggauagcuggaucacacccuug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3 AAC64407	AAC64407 Human Nog
2	25	100.0	75	9 ACC81049	ACC81049 Human Nog
3	25	100.0	75	9 ACC81057	ACC81057 Human Nog
4	25	100.0	90	9 ACC81058	ACC81058 Human Nog
5	25	100.0	105	9 ACC81059	ACC81059 Human Nog
6	25	100.0	120	9 ACC81054	ACC81054 Human Nog
7	25	100.0	198	9 ACC81055	ACC81055 Human Nog
8	25	100.0	198	9 ACC81056	ACC81056 Human Nog
9	25	100.0	198	12 ADQ16424	ADQ16424 Nucleotid
10	25	100.0	198	12 ADQ16424	ADQ16424 Nucleotid
11	25	100.0	261	2 AAV23697	AAV23697 Human NSP
12	25	100.0	404	2 AAX41193	AAX41193 Human sec
13	25	100.0	600	4 AAF90323	AAF90323 Human NOG
14	25	100.0	639	6 ABN96987	ABN96987 Gene #348
15	25	100.0	668	6 ABL89601	ABL89601 Human pol
16	25	100.0	770	3 AAV72983	AAV72983 Human NSP
17	25	100.0	799	2 AAV23695	AAV23695 Human NSP
18	25	100.0	991	2 AAX97587	AAX97587 Extended
19	25	100.0	994	12 ADP18854	ADP18854 Human sec
20	25	100.0	1122	3 AAZ56888	AAZ56888 Human MAG

C 21	25	100.0	1122	4 AAF90325	AAF90325 Human NOG
C 22	25	100.0	1213	2 AAX04379	AAX04379 Human sec
C 23	25	100.0	1216	6 ABA05903	ABA05903 Human RTN
C 24	25	100.0	1514	6 ABK34580	ABK34580 Human CDN
C 25	25	100.0	1599	10 ADI62860	ADI62860 Human apo
C 26	25	100.0	1610	3 AAZ36230	AAZ36230 cDNA enco
C 27	25	100.0	1683	4 AAD08386	AAD08386 Human sec
C 28	25	100.0	1694	4 AAK94408	AAK94408 Human ful
C 29	25	100.0	1694	12 ADL31137	ADL31137 Full leng
C 30	25	100.0	1758	4 AAF32725	AAF32725 Human sec
C 31	25	100.0	1785	12 ADK14166	ADK14166 Human aut
C 32	25	100.0	1798	6 ABK90135	ABK90135 DNA enco
C 33	25	100.0	1980	4 AAI98079	AAI98079 Human neu
C 34	25	100.0	2052	6 ABK90133	ABK90133 DNA enco
C 35	25	100.0	2235	6 ABV94681	ABV94681 Human pan
C 36	25	100.0	2240	3 AAC64406	AAC64406 Human NOG
C 37	25	100.0	2386	2 AAV30920	AAV30920 Human sec
C 38	25	100.0	2386	5 AAF98399	AAF98399 Human CDN
C 39	25	100.0	2610	11 ADI31056	ADI31056 Human CDN
C 40	25	100.0	2934	12 ADQ16433	ADQ16433 Construct
C 41	25	100.0	3579	3 AAZ56886	AAZ56886 Human MAG
C 42	25	100.0	3579	4 AAF90324	AAF90324 Human NOG
C 43	25	100.0	3579	6 ABK90134	ABK90134 DNA enco
C 44	25	100.0	3579	6 ABN86601	ABN86601 Human neu
C 45	25	100.0	3579	12 ADO07886	ADO07886 Human pol

ALIGNMENTS

RESULT 1

AAC64407

ID AAC64407 standard; RNA; 25 BP.

XX AAC64407;

DT 08-FEB-2001 (first entry)

XX

Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:3.

Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
stress-phosphorylated endoplasmic reticulum protein; cytosolic;
gene therapy; cell growth; cellular stress response; neuron growth;
regulator of oxidative stress; inhibitor of neurite outgrowth;
axon regeneration; diagnosis; cancer; identification; antisense;
phosphorothioate; ss.

OS Homo sapiens.

XX

Key Location/Qualifiers

modified_base 1..25

FT /*tag= a

FT /note= "phosphorothioate linkages"

FT

XX WO2000060083-A1.

XX

XX 12-OCT-2000.

XX

XX 07-APR-2000; 2000WO-US009383.

XX

PR 08-APR-1999; 99US-0128372P.

PR

XX 21-JUN-1999; 99US-0140331P.

XX

PA (CHIR) CHIRON CORP.

XX

PI Wei D, Halenbeck R, Williams LT;

XX

XX WPI; 2000-665007/64.

DR

Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PT

XX

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic
 CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and
 CC is a modulator of the storage and exchange of calcium, cell growth and
 CC cellular stress response. It can: regulate oxidative stress; inhibit
 CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
 CC polypeptides and polynucleotides are useful for modulating stress levels
 CC and cellular stress-response, cell growth and viability, diagnosis and
 CC treatment of cancer, malignant growth and other Nogo B related diseases.
 CC Nogo B polypeptides are also useful to screen combinatorial libraries to
 CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
 CC are useful for affinity chromatography and distinguishing Nogo B
 CC polypeptides. The present sequence represents a human Nogo B
 CC phosphorothioate antisense oligonucleotide from the present invention

XX Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
 DB 1 CUGGAUAGCUUGGAUCACACCCUUG 25

RESULT 2

ACC81049/c
 ID ACC81049 standard; cDNA; 75 BP.

AC ACC81049;

DT 22-JUL-2003 (first entry)

XX Human Nogo receptor inhibitor Pepl cDNA.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..75

FT /*tag= a
 FT /product= "Human Nogo receptor inhibitor Pepl"
 FT /note= "No start/stop codon given"

XX WO2003031462-A2.

PN 17-APR-2003.

PD 04-OCT-2002; 2002WO-US032007.

PF 06-OCT-2001; 2001US-00972599.

XX (UYA) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

DR P-PSDB; ABR59668.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

XX Disclosure; Page 135; 148pp; English.

XX The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an Ngr protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention

SQ Sequence 75 BP; 25 A; 15 C; 18 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 75;
 Best Local Similarity 72.0%; Pred. No. 0.068;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25

DB 36 CTGGTAGCTTGGATCACCCCTTG 12

RESULT 3

ACC81057/c

ID ACC81057 standard; cDNA; 75 BP.

AC ACC81057;

DT 22-JUL-2003 (first entry)

XX Human NogoA partial gene #2.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..75

FT /*tag= a
 FT /product= "Partial human NogoA"
 FT /note= "No start/stop codon given"

XX WO2003031462-A2.

PN 17-APR-2003.

PD 04-OCT-2002; 2002WO-US032007.

PF 06-OCT-2001; 2001US-00972599.

XX (UYA) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

DR P-PSDB; ABR59676.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system

PT neuron, or in treating central nervous system disease, disorder or
 XX injury, e.g. spinal cord injury.

PS Disclosure; Page 139; 148pp; English.

CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NGR
 CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NGR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention

XX SQ Sequence 75 BP; 25 A; 16 C; 18 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 75;
 Best Local Similarity 72.0%; Pred. No. 0.068;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGAUCACACCCUUG 25
 DB 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 4
 ACC81058/c

ID ACC81058 standard; cDNA; 90 BP.

XX AC ACC81058;

XX DT 22-JUL-2003 (first entry)

XX DE Human NogoA partial gene #3.

XX KW Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..90

XX FT /*tag= a
 XX FT /product= "Partial human NogoA"
 XX FT /note= "No start/stop codon given"

XX PN WO2003031462-A2.

XX XX 17-APR-2003.

XX XX 04-OCT-2002; 2002WO-US032007.

XX XX 06-OCT-2001; 2001US-00972599.

XX PA (UYUA) UNIV YALE.

XX PI Strittmatter SM;

XX DR WPI; 2003-393433/37.

DR P-PSDB; ABR59677.

XX New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

XX PS Disclosure; Page 140; 148pp; English.

XX CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NGR
 CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NGR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention

XX SQ Sequence 90 BP; 29 A; 18 C; 21 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 90;
 Best Local Similarity 72.0%; Pred. NO. 0.07;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGAUCACACCCUUG 25
 DB 33 CTGGATAGCTTGGATCACCCTTG 9

RESULT 5
 ACC81059/c

ID ACC81059 standard; cDNA; 105 BP.

XX AC ACC81059;

XX DT 22-JUL-2003 (first entry)

XX DE Human NogoA partial gene #4.

XX KW Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..105

XX FT /*tag= a
 XX FT /product= "Partial human NogoA"
 XX FT /note= "No start/stop codon given"

XX PN WO2003031462-A2.

XX XX 17-APR-2003.

XX XX 04-OCT-2002; 2002WO-US032007.

XX XX 06-OCT-2001; 2001US-00972599.

XX PA (UYUA) UNIV YALE.

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XX Strittmatter SM;
XX WPI; 2003-393433/37.
XX P-PSDB; ABR59678.
XX
XX New human Nogo receptor polypeptides and nucleic acids, useful for
XX decreasing inhibition of axonal growth by a central nervous system
XX neuron, or in treating central nervous system disease, disorder or
XX injury, e.g. spinal cord injury.
XX
XX Disclosure; Page 140; 148pp; English.
XX
XX The invention relates to a novel nucleic acid encoding a polypeptide
XX comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl,
XX human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of Pl with
XX 1-20 conservative amino acid substitutions, and less than a complete CTS
XX domain, provided that a partial CTS domain, if present, consists of no
XX more than the first 39 consecutive residues. The nucleic acid of the
XX invention has neuroprotective activity. The polynucleotide may have a use
XX in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX axonal growth by a central nervous system (CNS) neuron. The Ngr
XX polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
XX dependent signal transduction in the central nervous system neuron may be
XX used in treating central nervous system disease, disorder or injury, e.g.
XX spinal cord injury. Expression of an Ngr protein may be associated with
XX inhibition of axonal regeneration following cranial, cerebral or spinal
XX trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX monophasic demyelination, encephalomyelitis, multifocal
XX leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX sequence is used in the exemplification of the invention
XX
XX Sequence 105 BP; 32 A; 19 C; 28 G; 26 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 9; Length 105;
XX Best Local Similarity 72.0%; Pred. No. 0.072;
XX Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACCCTTG 9
XX
RESULT 6
ACC81054/c
ID ACC81054 standard; cDNA; 120 BP.
XX
AC ACC81054;
XX
XX 22-JUL-2003 (first entry)
XX
DE Human Nogo receptor inhibitor Pep2-41 cDNA.
XX
XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
XX axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
XX cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
XX demyelinating disease; multiple sclerosis; monophasic demyelination;
XX encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..120
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XX /*tag= a
XX /product= "Human Nogo receptor inhibitor Pep2-41"
XX /note= "No start/stop codon given"
XX
XX WO2003031462-A2.
XX
XX 17-APR-2003.
XX
XX 04-OCT-2002; 2002WO-US032007.
XX

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XX 06-OCT-2001; 2001US-00972599.
XX (UYVA ) UNIV YALE.
XX Strittmatter SM;
XX
XX WPI; 2003-393433/37.
XX P-PSDB; ABR59673.
XX
XX New human Nogo receptor polypeptides and nucleic acids, useful for
XX decreasing inhibition of axonal growth by a central nervous system
XX neuron, or in treating central nervous system disease, disorder or
XX injury, e.g. spinal cord injury.
XX
XX Disclosure; Page 137; 148pp; English.
XX
XX The invention relates to a novel nucleic acid encoding a polypeptide
XX comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl,
XX human Nogo receptor (NGR) NTLRRCT domain), or residues 27-309 of Pl with
XX 1-20 conservative amino acid substitutions, and less than a complete CTS
XX domain, provided that a partial CTS domain, if present, consists of no
XX more than the first 39 consecutive residues. The nucleic acid of the
XX invention has neuroprotective activity. The polynucleotide may have a use
XX in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX axonal growth by a central nervous system (CNS) neuron. The Ngr
XX polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-
XX dependent signal transduction in the central nervous system neuron may be
XX used in treating central nervous system disease, disorder or injury, e.g.
XX spinal cord injury. Expression of an Ngr protein may be associated with
XX inhibition of axonal regeneration following cranial, cerebral or spinal
XX trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX sequence is used in the exemplification of the invention
XX
XX Sequence 120 BP; 38 A; 21 C; 30 G; 31 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 9; Length 120;
XX Best Local Similarity 72.0%; Pred. No. 0.073;
XX Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACCCTTG 9
XX
RESULT 7
ACC81055/c
ID ACC81055 standard; DNA; 198 BP.
XX
AC ACC81055;
XX
XX 22-JUL-2003 (first entry)
XX
DE Human Nogo receptor binding region DNA.
XX
XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;
XX axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
XX cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
XX demyelinating disease; multiple sclerosis; monophasic demyelination;
XX encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..198
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XX /*tag= a
XX /product= "Human Nogo receptor binding region"
XX /note= "No start/stop codon given"
XX
XX WO2003031462-A2.
XX

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XX PD 17-APR-2003.
XX XX
XX PF 04-OCT-2002; 2002WO-US032007.
XX XX
XX PR 06-OCT-2001; 2001US-00972599.
XX XX
XX PA (UYUA ) UNIV YALE.
XX FI Strittmatter SM;
XX DR WPI; 2003-393433/37.
XX DR P-PSDB; ABR59674.
XX XX
XX PT New human Nogo receptor polypeptides and nucleic acids, useful for
XX PT decreasing inhibition of axonal growth by a central nervous system
XX PT neuron, or in treating central nervous system disease, disorder or
XX PT injury, e.g. spinal cord injury.
XX PS Disclosure; Page 139; 148pp; English.
XX CC The invention relates to a novel nucleic acid encoding a polypeptide
XX CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
XX CC human Nogo receptor (NGR) NTLRRT domain), or residues 27-309 of P1 with
XX CC 1-20 conservative amino acid substitutions, and less than a complete CTS
XX CC domain, provided that a partial CTS domain, if present, consists of no
XX CC more than the first 39 consecutive residues. The nucleic acid of the
XX CC invention has neuroprotective activity. The polynucleotide may have a use
XX CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX CC axonal growth by a central nervous system (CNS) neuron. The NGR
XX CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
XX CC dependent signal transduction in the central nervous system neuron may be
XX CC used in treating central nervous system disease, disorder or injury, e.g.
XX CC spinal cord injury. Expression of an NGR protein may be associated with
XX CC inhibition of axonal regeneration following cranial, cerebral or spinal
XX CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX CC monophasic demyelination, encephalomyelitis, multifocal
XX CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX CC sequence is used in the exemplification of the invention
XX SQ Sequence 198 BP; 54 A; 36 C; 48 G; 60 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCTTGGATCACACCCCTTG 25
Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 8
ACC81056/c
ID ACC81056 standard; cDNA; 198 BP.
XX AC ACC81056;
XX XX
XX DT 22-JUL-2003 (first entry)
XX DE Human NogoA partial gene #1.
XX KW Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;
XX KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
XX KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
XX KW demyelinating disease; multiple sclerosis; monophasic demyelination;
XX KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
XX KW ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 1..198
XX FT /*tag= a

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PT FT /product= "Partial human NogoA"
XX FT /note= "No start/stop codon given"
XX PN WO2003031462-A2.
XX PD 17-APR-2003.
XX XX
XX PF 04-OCT-2002; 2002WO-US032007.
XX XX
XX PR 06-OCT-2001; 2001US-00972599.
XX XX
XX PA (UYUA ) UNIV YALE.
XX XX
XX FI Strittmatter SM;
XX DR WPI; 2003-393433/37.
XX DR P-PSDB; ABR59675.
XX XX
XX PT New human Nogo receptor polypeptides and nucleic acids, useful for
XX PT decreasing inhibition of axonal growth by a central nervous system
XX PT neuron, or in treating central nervous system disease, disorder or
XX PT injury, e.g. spinal cord injury.
XX PS Disclosure; Page 139; 148pp; English.
XX CC The invention relates to a novel nucleic acid encoding a polypeptide
XX CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
XX CC human Nogo receptor (NGR) NTLRRT domain), or residues 27-309 of P1 with
XX CC 1-20 conservative amino acid substitutions, and less than a complete CTS
XX CC domain, provided that a partial CTS domain, if present, consists of no
XX CC more than the first 39 consecutive residues. The nucleic acid of the
XX CC invention has neuroprotective activity. The polynucleotide may have a use
XX CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
XX CC axonal growth by a central nervous system (CNS) neuron. The NGR
XX CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-
XX CC dependent signal transduction in the central nervous system neuron may be
XX CC used in treating central nervous system disease, disorder or injury, e.g.
XX CC spinal cord injury. Expression of an NGR protein may be associated with
XX CC inhibition of axonal regeneration following cranial, cerebral or spinal
XX CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
XX CC monophasic demyelination, encephalomyelitis, multifocal
XX CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
XX CC sequence is used in the exemplification of the invention
XX SQ Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCTTGGATCACACCCCTTG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 9
ADQ16424/c
ID ADQ16424 standard; DNA; 198 BP.
XX AC ADQ16424;
XX XX
XX DT 09-SEP-2004 (first entry)
XX DE Nucleotide sequence of Nogo-66 domain b.
XX KW Nogo-66; MAG; myelin protein; Nogo; glycoprotein; tenascin-R; TN-R;
XX KW TNR-BGFL; myelin-associated glycoprotein; neural growth;
XX KW central nervous system damage; CNS damage; spinal cord injury; stroke;
XX KW vaccine; myelin antigen; gene; ss.
XX OS Homo sapiens.
XX PN WO2004052922-A2.

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XX PD 24-JUN-2004.
XX PF
XX PF 05-DEC-2003; 2003WO-GB005323.
XX PR 06-DEC-2002; 2002US-0431620P.
XX PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
XX PA (DENI/) DENISON C M.
XX PI Xiao Z;
XX DR WPI; 2004-468911/44.
XX DR P-PSDB; ADQ16419.
XX PT New peptides that interact with myelin proteins Nogo, TNF and MAG, useful
XX PT in preparing a composition for treating CNS damage, spinal cord injury or
XX PT stroke.
XX PS Disclosure; SEQ ID NO 16; 81pp; English.
XX CC The present sequence encodes Nogo-66 domain b. The specification
XX CC describes peptides which interact with the myelin proteins Nogo
XX CC (specifically the Nogo-66 domain), the extracellular matrix glycoprotein
XX CC tenascin-R (TN-R) (specifically TN-R epidermal growth factor like (TNR-
XX CC EGFL)) and myelin-associated glycoprotein (MAG). These proteins have
XX CC neural growth inhibitory activity. The peptide is isolated from a 7-mer
XX CC phase display library exposed to a plate coated with the target protein.
XX CC Peptides of the invention are useful in preparing a composition for
XX CC treating central nervous system (CNS) damage, spinal cord injury or
XX CC stroke. The peptides may also be used in vaccines against myelin
XX CC antigens. The vaccine is based on the specific inhibitory portions of
XX CC major myelin proteins, instead of the whole protein.
XX SQ Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
DB 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 10
ADRI13967/c
ID ADRI13967 standard; cDNA; 198 BP.
XX AC ADRI13967;
XX DT 23-SEP-2004 (first entry)
XX DE Human Nogo-66 cDNA.
XX KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;
XX KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;
XX KW multiple system atrophy; Lou Gehrig's disease;
XX KW progressive supranuclear palsy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..198
XX FT /*tag= a
XX FT /partial
XX FT /product= "Nogo-66"
XX FT /note= "No start and stop codons given"
XX PN US2004121341-A1.
XX XX

```

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PD 24-JUN-2004.
XX PF
XX PF 20-DEC-2002; 2002US-00327213.
XX PR 20-DEC-2002; 2002US-00327213.
XX PA (FILB/) FILBIN M T.
XX PA (DOME/) DOMENICONI M.
XX PA (CAOZ/) CAO Z.
XX PI Filbin MT, Domeniconi M, Cao Z;
XX DR WPI; 2004-479666/45.
XX DR P-PSDB; ADRI13968.
XX PT New myelin-associated glycoprotein (MAG) derivative comprises a mutation
XX PT in or flanking MAG Ig-like domain 5 (IgD5), excluding the MAG derivative
XX PT MAG (dl-3)-Fc, useful promoting neural growth and regeneration.
XX PS Disclosure; SEQ ID NO 10; 81pp; English.
XX CC The invention relates to a myelin-associated glycoprotein (MAG)
XX CC derivative comprising a mutation in or flanking MAG Ig-like domain 5
XX CC (IgD5), excluding the MAG derivative MAG (dl-3)-Fc, where the mutation
XX CC reduces or eliminates the ability of the derivative to regulate neurite
XX CC outgrowth as compared to endogenous or soluble MAG without eliminating
XX CC binding to neuronal surfaces. The inhibitors of MAG are useful for
XX CC promoting neural growth and regeneration. They are also useful for
XX CC treating neural degeneration associated with injuries, disorders, or
XX CC diseases. The disorder, disease, or condition is associated with
XX CC apoptosis or results from a demyelinating disease and includes
XX CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
XX CC Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,
XX CC kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou
XX CC Gehrig's disease), or progressive supranuclear palsy. The present
XX CC sequence represents the human Nogo-66 cDNA.
XX SQ Sequence 198 BP; 56 A; 36 C; 49 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.079;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
DB 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 11
AAV23697/c
ID AAV23697 standard; cDNA; 261 BP.
XX AC AAV23697;
XX DT 24-JUL-1998 (first entry)
XX DE Human NSPLP protein coding sequence fragment.
XX KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
XX KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
XX OS Homo sapiens.
XX PN WO9806841-A2.
XX FT 19-FEB-1998.
XX PF 24-JUL-1997; 97WO-US013469.
XX PR 12-AUG-1996; 96US-00700607.
XX PA (INCY-) INCYTE PHARM INC.
XX XX

```

PI Bandman O, Au-Young J, Goli SK, Hillman J;
 XX WPI; 1998-159533/14.
 XX Human neuro-endocrine-specific protein-like proteins - useful for
 PT diagnosis, monitoring and treatment of cancer and neuro-degenerative
 PT disease.
 XX
 PS Disclosure; Page 45; 73pp; English.
 XX
 CC This sequence encodes a human neuroendocrine-specific protein-like
 CC protein (NSPLP) of the invention. Recombinant cells transformed with the
 CC DNA are used to express the NSPLP proteins, which are used to treat
 CC cancer and neurodegenerative diseases such as amyotrophic lateral
 CC sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
 CC used to inhibit activity of the NSPLP proteins. Antibodies specific for
 CC NSPLP are used for diagnosis and monitoring treatment of diseases
 CC associated with NSPLP expression, in usual immunoassays, and to isolate
 CC NSPLP from natural sources. The NSPLP proteins, or their fragments can
 CC also be used in drug screening to identify NSPLP antagonists. The nucleic
 CC acid can be used diagnostically and for monitoring treatment (in
 CC hybridisation or amplification assays); to isolate closely related
 CC sequences; in gene therapy for both sense and antisense applications
 CC (including use of ribozymes) and for mapping the natural genomic sequence
 XX
 SQ Sequence 261 BP; 62 A; 59 C; 56 G; 67 T; 0 U; 17 Other;
 Query Match 100.0%; Score 25; DB 2; Length 261;
 Best Local Similarity 72.0%; Pred. No. 0.082;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUGGAUAGCUUGGAUACACACCCUUG 25
 Db 124 CTGGATAGCTTGGATCACCACCCCTTG 100
 RESULT 12
 AAX41193/c
 ID AAX41193 standard; cDNA; 404 BP.
 AC AAX41193;
 XX
 DT 17-JUN-1999 (first entry)
 DE Human secreted protein 5' EST SEQ ID NO:137.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO9906548-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB001222.
 XX
 PR 01-AUG-1997; 97US-00905135.
 XX
 PA (GEST) GENSET.
 XX
 FI Dumas Milne Edwards J, Duclert A, Lacroix B;
 XX
 DR WPI; 1999-153778/13.
 DR P-PSDB; AAY12360.
 XX
 PT New nucleic acids encoding human secreted proteins - obtained from cDNA
 PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
 PT umbilical cord, placenta and colon tissue.

XX
 PS Claim 1; Page 319; 824pp; English.
 XX
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12261 to
 CC AAY12514, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell
 XX
 SQ Sequence 404 BP; 110 A; 75 C; 108 G; 111 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 2; Length 404;
 Best Local Similarity 72.0%; Pred. No. 0.088;
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUGGAUAGCUUGGAUACACACCCUUG 25
 Db 347 CTGGATAGCTTGGATCACCACCCCTTG 323
 RESULT 13
 AAF90323/c
 ID AAF90323 standard; cDNA; 600 BP.
 XX
 AC AAF90323;
 XX
 DT 23-JUL-2001 (first entry)
 DE Human NOGO-C cDNA.
 XX
 KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200136631-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 14-NOV-2000; 2000WO-GB004345.
 XX
 PR 15-NOV-1999; 99GB-00026995.
 PR 24-JAN-2000; 2000GB-00001550.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 FI Michalovich D, Prinjha R;
 XX
 DR WPI; 2001-343822/36.
 DR P-PSDB; AAB82348.
 XX
 PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
 PT gene and may be useful in the treatment of neural disorders including
 PT Alzheimer's and Parkinson's diseases.
 XX
 PS Claim 1; Page 25; 25pp; English.
 XX
 CC The present sequence is that of cDNA encoding human NOGO-C (see

CC AAB2348). NOGO-C is a novel splice variant of the human NOGO gene on
CC chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have
CC previously been identified. The invention provides NOGO-C polypeptides
CC and polynucleotides, and methods for producing such polypeptides by
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C
CC polypeptides and polynucleotides in the treatment of diseases including
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for use in
CC treating conditions associated with NOGO-C imbalance, and diagnostic
CC assays for detecting diseases associated with inappropriate NOGO-C
CC activity or levels
XX
SQ Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 600;
Best Local Similarity 72.0%; Pred. No. 0.093;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 216 CTGGATAGCTTGGATCACCCTTG 192
|:|||||:|||||:|||||:|

RESULT 14
ABL96987/c
ID ABL96987 standard; DNA; 639 BP.
XX
AC ABL96987;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3485 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
FN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 3485; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data

CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 639 BP; 138 A; 114 C; 149 G; 147 T; 0 U; 91 Other;

Query Match 100.0%; Score 25; DB 6; Length 639;
Best Local Similarity 72.0%; Pred. No. 0.094;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 415 CTGGATAGCTTGGATCACCCTTG 391
|:|||||:|||||:|||||:|

RESULT 15
ABL9601/c
ID ABL9601 standard; cDNA; 668 BP.
XX
AC ABL9601;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 163.
XX
KW Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89192.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 4; SEQ ID NO 163; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

Qy 1 CUGGAUAGCUUGGAUACACACCCUUG 25
Db 430 CTGGATAGCTTGGATCACACCCCTTG 406

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:00:21 ; Search time 731.757 Seconds
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1655.441 Million cell updates/sec

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Perfect score: 25
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	25	100.0	75	6 AX195251	AX195251 Sequence
C 2	25	100.0	120	6 AX195261	AX195261 Sequence
C 3	25	100.0	198	6 CQ827995	CQ827995 Sequence
C 4	25	100.0	198	6 AX195263	AX195263 Sequence
C 5	25	100.0	261	6 AR028524	AR028524 Sequence
C 6	25	100.0	404	6 BD076183	BD076183 5' EST of
C 7	25	100.0	600	9 HSA251385	AJ251385 Homo sapi
C 8	25	100.0	639	6 AX410838	AX410838 Sequence
C 9	25	100.0	799	6 AR028522	AR028522 Sequence
C 10	25	100.0	994	6 BD139293	BD139293 Extended
C 11	25	100.0	1079	9 BC007109	BC007109 Homo sapi
C 12	25	100.0	1122	6 BD249448	BD249448 Protein B
C 13	25	100.0	1122	9 HSA251384	AJ251384 Homo sapi
C 14	25	100.0	1151	9 BC001035	BC001035 Homo sapi
C 15	25	100.0	1213	6 BD194907	BD194907 86 human
C 16	25	100.0	1213	6 CQ855235	CQ855235 Sequence
C 17	25	100.0	1466	9 BC071848	BC071848 Homo sapi
C 18	25	100.0	1485	9 BC010737	BC010737 Homo sapi
C 19	25	100.0	1525	9 AK130812	AK130812 Homo sapi

C 20	25	100.0	1599	6 CQ769577	CQ769577 Sequence
C 21	25	100.0	1610	6 BD231889	BD231889 Bone marr
C 22	25	100.0	1617	9 AF087901	AF087901 Homo sapi
C 23	25	100.0	1619	9 AK129806	AK129806 Homo sapi
C 24	25	100.0	1654	9 BC012619	BC012619 Homo sapi
C 25	25	100.0	1668	9 BC026788	BC026788 Homo sapi
C 26	25	100.0	1691	9 AF132048	AF132048 Homo sapi
C 27	25	100.0	1694	6 CQ783030	CQ783030 Sequence
C 28	25	100.0	1694	6 BD127437	BD127437 Primer fo
C 29	25	100.0	1694	9 AK075039	AK075039 Homo sapi
C 30	25	100.0	1698	9 BC014366	BC014366 Homo sapi
C 31	25	100.0	1700	9 AF177332	AF177332 Homo sapi
C 32	25	100.0	1709	9 AB040463	AB040463 Homo sapi
C 33	25	100.0	1728	9 BC068991	BC068991 Homo sapi
C 34	25	100.0	1784	9 BC016165	BC016165 Homo sapi
C 35	25	100.0	1800	9 AY102276	AY102276 Homo sapi
C 36	25	100.0	1800	6 BD083733	BD083733 Nucleic a
C 37	25	100.0	1980	6 BD097380	BD097380 Nucleic a
C 38	25	100.0	2052	9 AB015639	AB015639 Homo sapi
C 39	25	100.0	2235	9 AF148538	AF148538 Homo sapi
C 40	25	100.0	2276	9 AF132047	AF132047 Homo sapi
C 41	25	100.0	2332	9 AY102277	AY102277 Homo sapi
C 42	25	100.0	2386	6 BD190738	BD190738 Secretd
C 43	25	100.0	2386	6 AX099401	AX099401 Sequence
C 44	25	100.0	2389	9 AY102278	AY102278 Homo sapi
C 45	25	100.0	2481	9 AF063601	AF063601 Homo sapi

ALIGNMENTS

RESULT 1
AX195251/c
LOCUS AX195251 75 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 7 from Patent WO0151520.
ACCESSION AX195251
VERSION AX195251.1 GI:15385811
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Strittmatter, S.M.
TITLE Nogo receptor-mediated blockade of axonal growth
JOURNAL Patent: WO 0151520-A 7 19-JUL-2001;
YALE UNIVERSITY (US)
FEATURES
source Location/Qualifiers
source 1..75
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="cDNA encoding receptor binding inhibitor Pepl"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 75;
Best Local Similarity 72.0%; Pred. No. 0.13;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGATAGCTTGGATCACCCTTG 12
RESULT 2
AX195261/c
LOCUS AX195261 120 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 17 from Patent WO0151520.
ACCESSION AX195261
VERSION AX195261.1 GI:15385815
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

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[illegible]

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QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
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Db 216 CTGGATAGCTTGGATCACACCCCTTG 192

RESULT 8
AX410838/c
LOCUS AX410838 639 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3485 from Patent WO0229103.
ACCESSION AX410838
VERSION AX410838.1 GI:21443543
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3485 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
    source
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
    /note="EMBL/GenBank Accession No. W27023"
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Query Match 100.0%; Score 25; DB 6; Length 639;
Best Local Similarity 72.0%; Pred. No. 0.15;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   :||||:||||:||||:||||:||||:|
Db 415 CTGGATAGCTTGGATCACACCCCTTG 391

RESULT 9
AR028522/c
LOCUS AR028522 799 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5858708.
ACCESSION AR028522
VERSION AR028522.1 GI:5940495
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.I.
TITLE Polynucleotides encoding two novel human neuroendocrine-specific
        proteins
JOURNAL Patent: US 5858708-A 2 12-JAN-1999;
FEATURES
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    1..799
    /organism="unknown"
    /mol_type="unassigned DNA"
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Query Match 100.0%; Score 25; DB 6; Length 799;
Best Local Similarity 72.0%; Pred. No. 0.15;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
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Db 290 CTGGATAGCTTGGATCACACCCCTTG 266

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BD139293/c
LOCUS BD139293 994 bp DNA linear PAT 18-SEP-2002
DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139293

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VERSION B0139293.1 GI:23234238
KEYWORDS JP 2002508182-A/45.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE Extended cDNA of secretory protein
JOURNAL Patent: JP 2002508182-A 45 19-MAR-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002508182-A/45
PD 19-MAR-2002
PF 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC score 8.6
CC seq ASUFLLSLTVFS/IV
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DEFINITION Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone
IMAGE:4291127), complete cds.
ACCESSION BC007109
VERSION BC007109.1 GI:13937989
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Carninci,P., Prange,C., Raha,S.S., Iqbalan,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2561.15 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_hic.*

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6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 22	25	100.0	388	1	AA192599 zq01f08.r
C 23	25	100.0	395	1	AV729281 AV729281
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C 27	25	100.0	410	1	AU297299	AU297299 AU297299
C 28	25	100.0	413	5	BX497982	BX497982 DFE2p779M
C 29	25	100.0	416	1	AA088462	AA088462 z182b09.r
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C 31	25	100.0	417	7	N55351	N55351 YV47d08.s1
C 32	25	100.0	418	2	BE694253	BE694253 QV2-BT068
C 33	25	100.0	423	6	C15922	C15922 C15922 Clon
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C 35	25	100.0	436	2	BE080786	BE080786 QV1-BT063
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C 37	25	100.0	440	7	CR558096	CR558096 DFE2p459M
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ALIGNMENTS

RESULT 1

CB295964/c

LOCUS

DEFINITION

220010 rev_1_G08_r_056.abl Chimpanzee brain library Koo's Pan

troglydotes CDNA clone 220010 rev_1_G08_r_056.abl 5', similar to

human RTN4 neuroendocrine-specific protein C like (foccon), mRNA

sequence.

ACCESSION

CB295964

VERSION

CB295964.1 GI:28621394

KEYWORDS

EST.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

REFERENCE

1 (bases 1 to 147)

AUTHORS

Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and

Paabo, S.

TITLE

Selection on human genes as revealed by comparisons to chimpanzee

CDNA

JOURNAL

Genome Res. (2003) In press

COMMENT

Contact: Paabo S

Evolutionary Genetics

Max-Planck-Institute for evolutionary Anthropology

Deutscher Platz 6, 04103 Leipzig, Germany

Tel: +49- (0)-341-3550 500

Fax: +49- (0)-341-3550 555

Email: paabo@eva.mpg.de

Seq primer: M13 reverse.

Location/Qualifiers

1. 147

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/clone="220010_rev_1_G08_r_056.abl"

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/lab_host="adult"

/clone_lib="Epicurian Coli (TM) XL-10-Gold"

/note="Vector: pUCHi; Site 1: Sfil-A, Site 2: Sfil-B; The

library was prepared using the SMART cDNA library

construction kit (Clontech), doing only primer extension,

but not PCR amplification of the cDNA. The only deviation

from the published protocol was that we cloned the cDNA

into a plasmid vector."

ORIGIN

Tel: 86 10 62091454
 Email: to_zl@msn.com

Query Match 100.0%; Score 25; DB 1; Length 257;
Best Local Similarity 72.0%; Pred. No. 0.63;
Matches 18: Conservative 7; Mismatches 0; Indels

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Human	Homo sapiens
Human	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 274)	
REFERENCE	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE	Short-run sequencing of the human transcriptome with ORF expressed

TITLE	Shimpon,A.O. Shogun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP Brazil Tel.: +55-11-2704922

Fax: +353-21-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?i=1&t=QV1-BT0631-180>)
 200-078-f05&t3=2000-02-18&t4=1
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 High quality sequence start: 8
 High quality sequence stop: 274.

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/dev_stage="Adult"
/Clone_lib="Br031"
/note="Organ: breast; Vector: puc18; Site 1: Smal; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORNSTE PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

```

ORIGIN

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Query Match      100.0%; Score 25; DB 2; Length 274;
Best Local Similarity 72.0%; Pred.NC. 0.64;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCAACCCUUG 25
    C T G G A U A G C U U G G A U C A C A C C C U U G
Db 167 C T G G A T A G C T T G G A T C A C A C C C T T G 143

```

RESULT 7	CF125576/c
LOCUS	CF125576
DEFINITION	UI-HF-EL0-avo-a-06-0-UI.r2 NIH_MGC_212 Homo sapiens linear mRNA 280 bp EST 05-AUG-2003
	IMAGE:30563621 5', mRNA sequence.

ACCESSION	CF125576
VERSION	CF125576.1
KEYWORDS	GI:33201944
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 280)
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.
	Normalization and subtraction: two approaches to facilitate gene
JOURNAL	discovery
MEDLINE	Genome Res. 6 (9), 791-806 (1996)
PUBMED	97044477
COMMENT	8889548
	Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>

```

seq primer: pYX-3, pYX-4
Location/Qualifiers
1..280
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30563621"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH MGC 212"
/notes="Organ: Lung; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bonafido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCC. Tissue was provided by Mary Hendrix."
```

ORIGIN

```
Query Match      100.0%; Score 25; DB 7; Length 280;
Best Local Similarity 72.0%; Pred. NO. 0.64;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8	BU073029/c	BU073029	286 bp	mrna	linear	EST 27-AUG-2002
LOCUS		im29a06.y1		Human insulinoma	cdna	Clone IMAGE:6036371
DEFINITION		5' similar to TR:Q9Y2Y7 Q9Y2Y7 POCEN-W. [2] TR:O94962 ;, mRNA sequence.				

ACCESSION	BU073029	
VERSION	BU073029.1	GI:22514218
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 286)

REFERENCE
AUTHORS
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemshko, I., Scearc, M., Brestell, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blaisdin, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.

TITLE	COMMENT
Endocrine Pancreas Consortium	
Other ESTs: im29a06.x1	
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue	
Endocrine Pancreas Consortium	
Harvard University, Howard Hughes Medical Institute	
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138	

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochp.harvard.edu
Library was constructed by Dr. J. Perter In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -402bp from Gibco.

FEATURES	SOURCE
-----------------	---------------

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1. .296
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6036371"
/tissue_type="insulinoma"
/lab_host="PH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/notes="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda\_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

```

ORIGIN

Query Match	100.0%;	Score 25;	DB 5;	Length 286;
Best Local Similarity	72.0%;	Pred. No. 0.64;		
Matches 18;	Conservative	7;	Mismatches	0;
			Indels	0;
			Gaps	0;

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QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 151 CTGGATAGCTTGGATCACCACCTTG 127

RESULT 9
BQ311462/c
LOCUS BQ311462 288 bp mRNA linear EST 16-MAY-2002
DEFINITION QV4-BN0090-070600-249-g10 BN0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ311462
VERSION BQ311462.1 GI:20867010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 288)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-BN0090-
070600-249-g10&t3=2000-06-07&t4=1)
Seq primer: puc 18 forward.
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/organism="Homo sapiens"
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 100.0%; Score 25; DB 5; Length 288;
Best Local Similarity 72.0%; Pred. No. 0.64;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 216 CTGGATAGCTTGGATCACCACCTTG 192

RESULT 10
C14200/c
LOCUS C14200 297 bp mRNA linear EST 30-SEP-1996
DEFINITION C14200 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA
clone GEN-037D12 5', mRNA sequence.
ACCESSION C14200
VERSION C14200.1 GI:1568907

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 151 CTGGATAGCTTGGATCACCACCTTG 127

RESULT 11
BQ311462/c
LOCUS BQ311462 288 bp mRNA linear EST 16-MAY-2002
DEFINITION QV4-BN0090-070600-249-g10 BN0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ311462
VERSION BQ311462.1 GI:20867010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 310)
AUTHORS Claudio,J.O., Masih-Khan,E., Tang,H., Goncalves,J., Voralia,M.,
Li,Z.H., Nadeen,V., Cukerman,E., Francisco-Pabalan,O., Liew,C.C.,
Woodgett,J.R. and Stewart,A.K.
TITLE A molecular compendium of genes expressed in multiple myeloma
JOURNAL Blood 100 (6), 2175-2186 (2002)
MEDLINE 22188429
PUBMED 12200383
COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, MSG 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
Email: k.stewart@utoronto.ca
PCR Primers
FORWARD: 5'-GCCAAGCTCGAATTAACCTCACTCAAGG-3'
BACKWARD: 5'-CCAGTGAATGTATACGACTCACTATAGGCG-3'
Seq primer: 5'-GAAATTAACCTCACTCAAGG-3'.
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 297)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
Maekawa,H., Shin,S. and Nakamura,Y.
TITLE Unpublished (1995)
JOURNAL
COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
FEATURES
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Best Local Similarity 72.0%; Pred. No. 0.64;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 163 CTGGATAGCTTGGATCACCACCTTG 139

RESULT 11
BQ311462/c
LOCUS BQ311462 288 bp mRNA linear EST 23-MAR-2001
DEFINITION QV4-BN0090-070600-249-g10 BN0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ311462
VERSION BQ311462.1 GI:13439413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 310)
AUTHORS Claudio,J.O., Masih-Khan,E., Tang,H., Goncalves,J., Voralia,M.,
Li,Z.H., Nadeen,V., Cukerman,E., Francisco-Pabalan,O., Liew,C.C.,
Woodgett,J.R. and Stewart,A.K.
TITLE A molecular compendium of genes expressed in multiple myeloma
JOURNAL Blood 100 (6), 2175-2186 (2002)
MEDLINE 22188429
PUBMED 12200383
COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, MSG 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
Email: k.stewart@utoronto.ca
PCR Primers
FORWARD: 5'-GCCAAGCTCGAATTAACCTCACTCAAGG-3'
BACKWARD: 5'-CCAGTGAATGTATACGACTCACTATAGGCG-3'
Seq primer: 5'-GAAATTAACCTCACTCAAGG-3'.
FEATURES
source
1..310
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/tissue_type="Blood"
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/dev stage="multiple myeloma"
/clone_lib="Myeloma (MVE) cDNA library"
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(T)18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MLV reverse transcriptase. To protect the cDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32P]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
EcoRI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The cDNAs were then
size-fractionated using Sephacryl S-500 column and then
ligated into EcoRI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using Gigapack
II packaging extract. The library had primary titre of
approx. 1x106. Clones from the primary library were
randomly selected for single pass sequencing."

```

ORIGIN

```
Query Match      100.0%; Score 25; DB 2; Length 310;
Best Local Similarity 72.0%; Pred. No. 0.65;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CUGGAUAGCUUGGACACACACCCUUG 25
| : | : | : | : | : | : | : | : |
Db 111 CTGGATAGCTTGGATCACACCCCTTG 87

RESULT 12
CN429721/C

LOCUS	CN429721	327 bp	mrna	linear	EST 16-MAY-2004
DEFINITION	17000600012780 GRN PRENEU Homo sapiens cdNA 5', mRNA sequence.				

DEFINITION	170006000012780 GRN_FREN_
ACCESSION	CN429721
VERSION	CN429721.1 GI:47417315

KEYWORDS EST.
SOURCE Homo sapiens (human)

SOURCE	HOMO SAPIENS (human)
ORGANISM	Homo sapiens

ORGANISM: *Homo sapiens*
Eukaryota: Metazoa:

Eukaryota; Metazoa;
Mammalia: Eutheria:

REFERENCE
1 (bases 1 to 327)
Mammalia; Eutheria;

REFERENCE
AITHOPS
Brandenburger P We
I (bases 1 to 327)

AUTHORS

Li, Y., Xu, C., Fang, R.

Lebkowski, J and Stan

TITLE Transcriptional characterization of the

control human ES cell

JOURNAL Nat. Biotechnol. 22

COMMENT
Contact: Brandenburg

Regenerative Medicine

Geron Corporation

230 Constitution Drive

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberge@uconn.edu

Insert Length: 327

FEATURES

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conditions.
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ORIGIN

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-BN0148-0501>)
Seq primer: puc 18 forward
500-215-d09&t3=2000-05-05&t4=1
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High quality sequence stop: 345.

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1. 346
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/dev_stage="Adult"
/clone_lib="BN0148"
/note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

```

Query Match      100.0%; Score 25; DB 2; Length 346;
Best Local Similarity 72.0%; Pred. No. 0.66;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

y 1 CUGGAUACUUGGAUACACCCUUG 25
   |||:|||||:|||||:|
b 328 CTGATAGCTTGGATCACACCTTG 304

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Search completed: July 30, 2005, 15:00:58
Job time : 2564.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggauagcuggaucacacccuug 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	261	2	US-08-700-607-9
C 2	25	100.0	601	4	US-09-949-016-117588
C 3	25	100.0	601	4	US-09-949-016-117589
C 4	25	100.0	799	2	US-08-700-607-2
C 5	25	100.0	1669	4	US-09-949-016-3253
C 6	25	100.0	2610	4	US-09-023-655-382
C 7	25	100.0	4822	3	US-09-484-970B-106
C 8	25	100.0	42075	4	US-09-949-016-14995
C 9	18.6	74.4	175236	4	US-09-949-016-14353
C 10	18.2	72.8	601	4	US-09-949-016-167886
C 11	18.2	72.8	1593	3	US-09-676-610B-25
C 12	18.2	72.8	1868	1	US-08-658-883B-1
C 13	18.2	72.8	1868	3	US-09-676-610B-26
C 14	18.2	72.8	3633	2	US-09-715-249-1
C 15	18.2	72.8	5532	2	US-08-475-035-3
C 16	18.2	72.8	5532	3	US-09-676-610B-17
C 17	18.2	72.8	63000	4	US-09-780-172-18
C 18	18.2	72.8	63926	4	US-09-949-016-16473
C 19	18.2	72.8	64626	4	US-09-949-016-12011
C 20	18.2	72.8	169998	3	US-09-676-610B-24
C 21	18.2	72.8	197496	4	US-09-877-177A-10
C 22	17.8	71.2	403	4	US-09-513-999C-1468
C 23	17.8	71.2	601	4	US-09-949-016-91585
C 24	17.8	71.2	601	4	US-09-949-016-91586
C 25	17.8	71.2	57837	4	US-09-949-016-14371
C 26	17.8	71.2	57839	4	US-09-949-016-17601
C 27	17.6	70.4	1227	4	US-09-710-279-2285

C 28	17.6	70.4	1557	3	US-09-134-001C-1907	Sequence 1907, Ap
C 29	17.6	70.4	3046	4	US-09-710-279-3782	Sequence 3782, Ap
C 30	17	68.0	226	4	US-09-621-376-16264	Sequence 16264, A
C 31	17	68.0	375	4	US-09-902-540-8294	Sequence 8294, Ap
C 32	17	68.0	601	4	US-09-949-016-25253	Sequence 25253, A
C 33	17	68.0	601	4	US-09-949-016-25254	Sequence 25254, A
C 34	17	68.0	601	4	US-09-949-016-26285	Sequence 26285, A
C 35	17	68.0	601	4	US-09-949-016-26286	Sequence 26286, A
C 36	17	68.0	601	4	US-09-949-016-26287	Sequence 26287, A
C 37	17	68.0	601	4	US-09-949-016-31105	Sequence 31105, A
C 38	17	68.0	601	4	US-09-949-016-31106	Sequence 31106, A
C 39	17	68.0	601	4	US-09-949-016-82471	Sequence 82471, A
C 40	17	68.0	601	4	US-09-949-016-116493	Sequence 116493, A
C 41	17	68.0	601	4	US-09-949-016-116511	Sequence 116511, A
C 42	17	68.0	601	4	US-09-949-016-124120	Sequence 124120, A
C 43	17	68.0	601	4	US-09-949-016-124121	Sequence 124121, A
C 44	17	68.0	601	4	US-09-949-016-142012	Sequence 142012, A
C 45	17	68.0	601	4	US-09-949-016-142013	Sequence 142013, A

ALIGNMENTS

RESULT 1

US-08-700-607-9/c
; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 28742
US-08-700-607-9

Query Match 100.0%; Score 25; DB 2; Length 261;
Best Local Similarity 72.0%; Pred. No. 0.015;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGAUCACACCCUUG 25


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; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253

Query Match      100.0%; Score 25; DB 4; Length 1669;
Best Local Similarity 72.0%; Pred. No. 0.02;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:|||||:|||||:|||||:|
Db 430 CTGGATAGCTTGGATCACACCCCTTG 406

RESULT 6
US-09-023-655-382/c
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
US-09-023-655-382

Query Match      100.0%; Score 25; DB 4; Length 2610;
Best Local Similarity 72.0%; Pred. No. 0.022;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:|||||:|||||:|||||:|
Db 1494 CTGGATAGCTTGGATCACACCCCTTG 1470

RESULT 7

US-09-484-970B-106/c
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match      100.0%; Score 25; DB 3; Length 4822;
Best Local Similarity 72.0%; Pred. No. 0.024;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:|||||:|||||:|||||:|
Db 3450 CTGGATAGCTTGGATCACACCCCTTG 3426

RESULT 8
US-09-949-016-14995/c
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995

Query Match      100.0%; Score 25; DB 4; Length 42075;
Best Local Similarity 72.0%; Pred. No. 0.034;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUUG 25
   |||:|||||:|||||:|||||:|
Db 24830 CTGGATAGCTTGGATCACACCCCTTG 24806

RESULT 9
US-09-949-016-14353
; Sequence 14353, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14353
; LENGTH: 175236
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14353

Query Match      74.4%; Score 18.6; DB 4; Length 175236;
Best Local Similarity 64.0%; Pred. No. 51;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGAUCACACCCUUG 25
Db 132015 CTGGATAGCTGGATCAGCGCATG 132039

RESULT 10
US-09-949-016-167886/c
; Sequence 167886, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167886
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-167886

Query Match      72.8%; Score 18.2; DB 4; Length 601;
Best Local Similarity 69.6%; Pred. No. 33;
Matches 16; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAUAGCUUGAUCACACCCUUG 25
Db 599 GGAGAGCTAGGATCAGCATTG 577

RESULT 11
US-09-676-610B-25/c
; Sequence 25, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
```

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; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 25
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)...(1462)
US-09-676-610B-25

Query Match      72.8%; Score 18.2; DB 3; Length 1593;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAUAGCUUGAUCACACCCUUG 25
Db 828 GGAGAGCTGGATCAGCATTG 806

RESULT 12
US-08-658-883B-1/c
; Sequence 1, Application US/08658883B
; Patent No. 5708156
; GENERAL INFORMATION:
; APPLICANT: Ilekis, John V.
; TITLE OF INVENTION: An Epidermal Growth Factor
; Receptor-like Gene Product and Its Uses
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John V. Ilekis
; STREET: 4206 Linden Avenue
; CITY: Western Springs
; STATE: IL
; COUNTRY: U.S.A
; ZIP: 60558
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft DOS 6.2
; SOFTWARE: Microsoft No. 5708156epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,883B
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5708156 Applicable
; FILING DATE: No. 5708156 Applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5708156 Applicable
; REGISTRATION NUMBER: No. 5708156 Applicable
; REFERENCE/DOCKET NUMBER: No. 5708156 Applicable
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-996-6273/708-246-9085
; TELEFAX: No. 5708156 Applicable
; TELEX: No. 5708156 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1868 bases
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Term Placenta
; IMMEDIATE SOURCE:
; LIBRARY: cDNA
; FEATURE:
; OTHER INFORMATION: Deduced amino acid length
; of 381. Putative signal peptide Met-1 to Ala-24.
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US-08-658-883B-1

Query Match 72.8%; Score 18.2; DB 1; Length 1868;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 1087 GGACAGCTTGGATCACACTTTTG 1065

RESULT 13

US-09-676-610B-26/c
; Sequence 26, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 26
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (504)...(1721)
US-09-676-610B-26

Query Match 72.8%; Score 18.2; DB 3; Length 1868;
Best Local Similarity 65.2%; Pred. No. 39;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 1087 GGACAGCTTGGATCACACTTTTG 1065

RESULT 14

US-09-715-249-1/c
; Sequence 1, Application US/09715249
; Patent No. 6790614
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; APPLICANT: VERES, GABOR
; APPLICANT: PIPPIG, SUSANNE
; TITLE OF INVENTION: selectable cell surface marker genes
; FILE REFERENCE: 4-31192
; CURRENT APPLICATION NUMBER: US/09/715.249
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: us 60/166594
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: us 09/539248
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: EGFR
US-09-715-249-1

Query Match 72.8%; Score 18.2; DB 4; Length 3633;
Best Local Similarity 65.2%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 584 GGACAGCTTGGATCACACTTTTG 562

RESULT 15

US-08-475-035-3/c
; Sequence 3, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
US-08-475-035-3

Query Match 72.8%; Score 18.2; DB 2; Length 5532;
Best Local Similarity 65.2%; Pred. No. 47;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGAUAGCUUGGAUCACACCCUUG 25
Db 770 GGACAGCTTGGATCACACTTTTG 748

Search completed: July 30, 2005, 15:05:35
Job time : 91.2027 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:00:21 ; Search time 731.757 Seconds
(without alignment)
1655.441 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20.8	83.2	182405	10	AC124978 Mus muscu
2	20.8	83.2	230629	10	AC127332 Mus muscu
3	20.4	81.6	27745	9	AF065393 Homo sapi
4	20.2	80.8	218922	5	AL029292 Zebrafish
5	19.8	79.2	89317	2	AC025121 Homo sapi
6	19.8	79.2	150154	9	AL391477 Human DNA
7	19.8	79.2	157280	2	AC022378 Homo sapi
8	19.4	77.6	1243	1	AY212597 Unculture
9	19.2	76.8	2423	4	AB028866 Bos tauru
10	19.2	76.8	40304	6	AX695905 Sequence
11	19.2	76.8	86574	6	CQ861540 Sequence
12	19.2	76.8	89566	9	AL390204 Human DNA
13	19.2	76.8	110000	2	AL672265
14	19.2	76.8	123325	8	AP006116
15	19.2	76.8	151851	2	AC009157 Homo sapi
16	19.2	76.8	163217	9	AF336797 Homo sapi
17	19.2	76.8	173627	9	AC099511 Homo sapi
18	19.2	76.8	179168	2	AC009071 Homo sapi
19	19.2	76.8	179168	2	AC009071 Homo sapi

C 20	19.2	76.8	195189	2	AC034149	AC034149 Homo sapi
C 21	19.2	76.8	279177	2	AC146652	AC146652 Pan trogl
C 22	18.8	75.2	106346	9	AC004045	AC004045 Homo sapi
C 23	18.8	75.2	153624	9	HS1018K9	AL031726 Human DNA
C 24	18.8	75.2	164736	2	AL390855	AL390855 Homo sapi
C 25	18.8	75.2	189876	2	AC084810	AC084810 Homo sapi
C 26	18.8	75.2	226791	2	AC094199	AC094199 Rattus no
C 27	18.8	75.2	227208	2	AC150218	AC150218 Callithri
C 28	18.6	74.4	10670	1	U32781	U32781 Haemophilus
C 29	18.6	74.4	63798	2	AC124310	AC124310 Homo sapi
C 30	18.6	74.4	110000	6	BD426631_10	Continuation (11 o
C 31	18.6	74.4	110000	6	AR274513_10	Continuation (11 o
C 32	18.6	74.4	110000	6	AR541453_10	Continuation (11 o
C 33	18.6	74.4	148326	2	AC103619	AC103619 Mus muscu
C 34	18.6	74.4	148344	10	AC090432	AC090432 Mus muscu
C 35	18.6	74.4	156997	9	AC011465	AC011465 Homo sapi
C 36	18.6	74.4	164291	9	AC021351	AC021351 Homo sapi
C 37	18.6	74.4	165408	2	AC122425	AC122425 Mus muscu
C 38	18.6	74.4	167167	2	AC012035	AC012035 Homo sapi
C 39	18.6	74.4	167550	2	EX296544	EX296544 Danio rer
C 40	18.6	74.4	170807	9	AC124307	AC124307 Homo sapi
C 41	18.6	74.4	171224	2	AC091600	AC091600 Homo sapi
C 42	18.6	74.4	177302	10	AC127415	AC127415 Mus muscu
C 43	18.6	74.4	183089	10	AL663115	AL663115 Mouse DNA
C 44	18.6	74.4	189650	10	AC136091	AC136091 Rattus no
C 45	18.6	74.4	191925	9	AC147386	AC147386 Pan trogl

ALIGNMENTS

RESULT 1	AC124978	182405 bp	DNA	linear	ROD 13-APR-2004
LOCUS	Mus musculus chromosome 5, clone RP24-107D19, complete sequence.				
DEFINITION	AC124978				
ACCESSION	AC124978.19	GI:46359995			
VERSION	HTG.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 182405)				
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.				
TITLE	Mus musculus chromosome 5, clone RP24-107D19				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 182405)				
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliiev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
REFERENCE	3 (bases 1 to 182405)				

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collamore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Minova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 182405)

JOURNAL

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collamore,A., Cook,A., Cooke,P., Corum,B.,
DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D.,
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Minova,T., Mienga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 13, 2004 this sequence version replaced gi:45268181.

All repeats were identified using RepeatMasker:

Smith, A.P.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: L24353

Center clone name: 107_D19

Some of the sequence contained within base pairs 96927 to the end
of the clone was stolen from accession ACL27332.

FEATURES

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/map="5"
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/clone_lib="RPCI-24 Male Mouse BAC"

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1..11787
/note="wgs_end_extension
clone end:SP6"
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844..11184
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4115..4167
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4234..4269
/rpt_family="(TA)n"
4394..4529
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4559..4606
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4634..4751
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4983..5074
/rpt_family="PB1D10"
5079..5473
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5474..6176
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5537..5570
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9384..9421
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complement(10594..10701)
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11603..11625
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11763..11881
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11788..11791
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14622..14740
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15412..15536
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15933..16065
/rpt_family="B1P"
complement(16149..16316)
/rpt_family="B3"

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repeat_region complement(16368..16516)
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repeat_region complement(16518..16557)
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repeat_region complement(17427..17641)
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/rpt_family="Lx2"
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/rpt_family="(AGGGGG)n"

Query Match 83.2%; Score 20.8; DB 10; Length 182405;
Best Local Similarity 70.8%; Pred. NO. 29;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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DB 119205 AACATCAGGATTCAGGTATGCC 119228

RESULT 2
AC127332/c AC127332 230629 bp DNA linear ROD 08-NOV-2003
DEFINITION Mus musculus BAC clone RP23-13611 from 5, complete sequence.
ACCESSION AC127332
VERSION AC127332.3 GI:29164695
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 230629)
Nguyen,C., Cotton,M., Meyer,R. and Haglund,K.
The sequence of Mus musculus BAC clone RP23-13611
REFERENCE 2 (bases 1 to 230629)
Wilson,R.
Sequencing of Mus musculus
Unpublished (2001)
REFERENCE 3 (bases 1 to 230629)
McPherson,J.D. and Waterston,R.H.
Direct Submision
Submitted (14-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 230629)
McPherson,J.D. and Waterston,R.H.
Direct Submision
Submitted (22-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 230629)
McPherson,J.D. and Waterston,R.H.
Direct Submision
Submitted (23-MAR-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 230629)
Wilson,R.
Direct Submision
Submitted (08-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 23, 2003 this sequence version replaced gi:27819587.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
-----
Center project name: M_BA0136101

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Oseigawa and Minako Tatenio in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES

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	/clone_lib="RPCI-23"
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154..261	
	/rpt_family="B4"
284..514	
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1641..1812	
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2833..2922	
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3625..3741	
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3912..4098	
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4551..4641	
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5100..5450	
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9338..9524	
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10096..10242	

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32732..33091
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39082..39735

Query Match 83.2%; Score 20.8; DB 10; Length 230629;
Best Local Similarity 70.8%; Pred. No. 30;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCCC 25
||| :||||:|||| :||||
Db 208425 AACATCAGGATTCAGGTATGCC 208402

RESULT 3
AF065393/c 27745 bp DNA linear PRI 26-JUN-1998
LOCUS AF065393
DEFINITION Homo sapiens cosmid 1F1, complete sequence.
ACCESSION AF065393
VERSION AF065393.1 GI:3253311
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 27745)
AUTHORS Gloeckner,G., Rosenthal,A. and Scherer,S.
TITLE Cosmid 1F1 of unknown origin containing G-binding protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 27745)
AUTHORS Gloeckner,G., Rosenthal,A., Drescher,B., Weber,J. and Schattevoy,R.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1998) Genome Analysis, Institut for Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE 3 (bases 1 to 27745)
AUTHORS Gloeckner,G., Rosenthal,A., Drescher,B., Weber,J. and Schattevoy,R.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Genome Analysis, Institut for Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REMARK TN1000 sequence removed by database staff
COMMENT On Jun 26, 1998 this sequence version replaced gi:3153872.
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gland NBMMG Mus musculus P = 9.9e-10 S = 350"
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604..682
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exon exon
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/evidence=not_experimental
/rpt_type=Inverted
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/note="I12 with 88% homology to I11"
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4854. .4886
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5101. .5105
/note="TN1000 insertion site in cosmid I1"
5185. .5190
/note="Genscan, score = 1.05%, comment = Length 6 bp"
/evidence=not_experimental
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/evidence=not_experimental
/rpt_family="AluSp"
5734. .5900
/evidence=not_experimental
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6364. .6448
/evidence=not_experimental
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Region: CpG island"
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23426. .23526,24675. .24767,26224. .26289,26892. .26957)
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TIEMQAITALAHRAAALYYMDLSEQQCGHGLKEQLFQNIPLFINKPLXVANKCD
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DLQKYDLMSSEKQDKIPELWEGHNVDYIDPAIMKAKQIREKKKULKILSKSKNTQ
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14339. .14409
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14545. .14645
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/rpt_type=tandem
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embryonic region Mus musculus P = 7.4e-23 S = 640"
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complement(17271. .17344)
/note="BLASTN2 (EST exons), 3:1F1.X.599.00 Ex 43 365. .438
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Query Match 81.6%; Score 20.4; DB 9; Length 27745;
 Best Local Similarity 68.2%; Pred. No. 43;
 Matches 15; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ACUCAGGAGUUCAGAUAGGCC 24
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 Db 6933 ACTTCAGGATTCAGATATGTC 6912

RESULT 4
 AL929292 218922 bp DNA linear VRT 23-SEP-2003
 Zebrafish DNA sequence from clone DKEY-11L24 in linkage group 14,
 complete sequence.
 ACCESSION AL929292 GI:34996460
 VERSION AL929292.7
 KEYWORDS HTG.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 218922)
 Direct Submission
 Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Sep 23, 2003 this sequence version replaced gi:28445772.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Title: SC
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep DKEY-11L24 is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5
 Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml.

FEATURES

source

1. .218922
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEY-11L24"
 /clone_lib="DanioKey"

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 218922;
 Best Local Similarity 68.0%; Pred. No. 60;
 Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAACUUCAGGAGUUCAGAUAGGCC 25
 |||:|||||:|||||:|
 Db 185663 CAACTTCAGCATTCAGAAATGCAC 185687

RESULT 5
 AC025121/c
 LOCUS AC025121
 DEFINITION Homo sapiens chromosome 1 clone RP11-21M14 map 1, LOW-PASS SEQUENCE SAMPLING.
 ACCESSION AC025121 GI:7158932
 VERSION AC025121.1
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 89317)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 1, clone RP11-21M14
 Unpublished
 2 (bases 1 to 89317)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castile,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieue,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stage-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L7580
 Center clone name: 21_M_14

* NOTE: This record contains 93 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that

* the record is updated, the accession number will
* be preserved.
1 854: contig of 854 bp in length
855 954: gap of 100 bp
956 1814: contig of 860 bp in length
957 1815: gap of 100 bp
1915 1914: contig of 840 bp in length
2755 2854: gap of 100 bp
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3812 4677: contig of 866 bp in length
4678 4777: gap of 100 bp
5478 5649: contig of 872 bp in length
5650 5749: gap of 100 bp
5750 6564: contig of 815 bp in length
6565 6664: gap of 100 bp
6665 7532: contig of 868 bp in length
7533 7632: gap of 100 bp
7633 8487: contig of 855 bp in length
8488 8587: gap of 100 bp
8588 9448: contig of 861 bp in length
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15209 15308: gap of 100 bp
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17071 17170: gap of 100 bp
17171 18065: contig of 895 bp in length
18066 18165: gap of 100 bp
18166 19042: contig of 877 bp in length
19043 19142: gap of 100 bp
19143 20003: contig of 861 bp in length
20004 20103: gap of 100 bp
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20958 21057: gap of 100 bp
21058 21929: contig of 872 bp in length
21930 22029: gap of 100 bp
22030 22876: contig of 847 bp in length
22877 22976: gap of 100 bp
22977 23845: contig of 869 bp in length
23846 23945: gap of 100 bp
23946 24812: contig of 867 bp in length
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24913 25784: contig of 872 bp in length
25785 25884: gap of 100 bp
25885 26758: contig of 874 bp in length
26759 26858: gap of 100 bp
26859 27731: contig of 873 bp in length
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27832 28698: contig of 867 bp in length
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28799 29662: contig of 864 bp in length
29663 29762: gap of 100 bp
29763 30639: contig of 877 bp in length
30640 30739: gap of 100 bp
30740 31570: contig of 831 bp in length
31571 31670: gap of 100 bp
31671 32532: contig of 862 bp in length
32533 32632: gap of 100 bp
32633 33511: contig of 879 bp in length
33512 33611: gap of 100 bp
33612 34496: contig of 885 bp in length

34497 34596: gap of 100 bp
34597 35461: contig of 865 bp in length
35462 35561: gap of 100 bp
35562 36403: contig of 842 bp in length
36404 36503: gap of 100 bp
36504 37377: contig of 874 bp in length
37378 37477: gap of 100 bp
37478 38342: contig of 865 bp in length
38343 38442: gap of 100 bp
38443 39310: contig of 868 bp in length
39311 39410: gap of 100 bp
39411 40279: contig of 869 bp in length
40280 40379: gap of 100 bp
40380 41245: contig of 866 bp in length
41246 41345: gap of 100 bp
41346 42196: contig of 851 bp in length
42197 42296: gap of 100 bp
42297 43117: contig of 821 bp in length
43118 43217: gap of 100 bp
43218 44089: contig of 872 bp in length
44090 44189: gap of 100 bp
44190 45041: contig of 852 bp in length
45042 45141: gap of 100 bp
45142 46012: contig of 871 bp in length
46013 46112: gap of 100 bp
46113 46962: contig of 850 bp in length
46963 47062: gap of 100 bp
47063 47926: contig of 864 bp in length
47927 48026: gap of 100 bp
48027 48889: contig of 863 bp in length
48890 48989: gap of 100 bp
48990 49860: contig of 871 bp in length
49861 49960: gap of 100 bp
49961 50821: contig of 861 bp in length
50822 50921: gap of 100 bp
50922 51783: contig of 862 bp in length
51784 51883: gap of 100 bp
51884 52736: contig of 853 bp in length
52737 52836: gap of 100 bp
52837 53700: contig of 864 bp in length
53701 53800: gap of 100 bp
53801 54665: contig of 865 bp in length
54666 54765: gap of 100 bp
54766 55687: contig of 922 bp in length
55688 55787: gap of 100 bp
55788 56623: contig of 836 bp in length
56624 56723: gap of 100 bp
56724 57590: contig of 867 bp in length
57591 57690: gap of 100 bp
57691 58550: contig of 860 bp in length
58551 58651: gap of 100 bp
58651 59526: contig of 876 bp in length
59527 59626: gap of 100 bp
59627 60506: contig of 880 bp in length
60507 60606: gap of 100 bp
60607 61469: contig of 863 bp in length
61470 61569: gap of 100 bp
61570 62438: contig of 869 bp in length
62439 62538: gap of 100 bp
62539 63364: contig of 826 bp in length
63365 63464: gap of 100 bp
63465 64326: contig of 862 bp in length
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64427 65281: contig of 855 bp in length
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Query Match 79.2%; Score 19.8; DB 2; Length 89317;
Best Local Similarity 69.6%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUUCAGAUAGGCC 24

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Db 13870 AACTTCAGGATTCAGAAATTC 13848
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RESULT 6
AL391477/c 150154 bp DNA linear PRI 17-JUL-2002
LOCUS Human DNA sequence from clone RP11-21M14 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL391477
VERSION AL391477.20 GI:21911468
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 150154)
JOURNAL Tromans,A.
COMMENT Direct Submission
Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 19, 2002 this sequence version replaced gi:21537432.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30) ; an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-21M14 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
FEATURES
source
1..150154
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone_lib="RP11-21M14"
/clone_lib="RPCI-11.1"

ORIGIN
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Best Local Similarity 69.6%; Pred. No. 94;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUUCAGGUAUCCAGAUUCC 24
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Db 120469 AACTTCAGGATTCAGAAATTC 120447
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QY 2 AACUUCAGGAUUCAGAUUGCC 24
Db 22869 AACTTCAGGATCCAGAAATCC 22891

RESULT 8
AY212597/c 1243 bp DNA linear BCT 16-JAN-2004
LOCUS Uncultured bacterium clone 146ds20 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY212597
VERSION AY212597.1 GI:37786996
KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1243)
AUTHORS Simpson,J.M., Santo Domingo,J.W. and Reasoner,D.J.
TITLE Assessment of equine fecal contamination: the search for
alternative bacterial source-tracking targets
JOURNAL FEMS Microbiol. Ecol. 47 (1), 65-75 (2004)
REFERENCE 2 (bases 1 to 1243)
AUTHORS Simpson,J.M., Santo Domingo,J.W. and Reasoner,D.J.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Office of Research and Development - Water
Supply Water Resources Division, U.S. Environmental Protection
Agency, 26 W. Martin Luther King Dr., Cincinnati, OH 45268, USA
FEATURES
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/organism="uncultured bacterium"
/mol_type="genomic DNA"
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/db_xref="taxon:77133"
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/product="16S ribosomal RNA"

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ORIGIN
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Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 15; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 CUUCAGGAUUCAGAUUGCC 24
Db 1001 CTTCAGGATCCAGATGCC 981

RESULT 9
AB028866/c 2423 bp mRNA linear MAM 17-JUN-1999
LOCUS Bos taurus mRNA for prollyl oligopeptidase, complete cds.
DEFINITION Bos taurus mRNA for prollyl oligopeptidase, complete cds.
ACCESSION AB028866
VERSION AB028866.1 GI:5103284
KEYWORDS prollyl oligopeptidase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Cloning and expression of the cDNA encoding prollyl oligopeptidase
JOURNAL Biol. Pharm. Bull. 20 (10), 1047-1050 (1997)
MEDLINE 98014979
PUBMED 9353562
REFERENCE 2 (bases 1 to 2423)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Direct Submission

QY 1 CAACUUCAGGAUUCAGAUUGCC 24
Db 956 CCACCTTCAGGATCCAGTGATGCC 933

RESULT 10
AX695905/c 40304 bp DNA linear PAT 31-MAR-2003
LOCUS AX695905
DEFINITION Sequence 1532 from Patent WO03008583.
ACCESSION AX695905
VERSION AX695905.1 GI:29419070
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morris,D.W. and Engelhard,E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 1532 30-JAN-2003;
Sagres Discovery (US)
FEATURES
source
1..40304
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 76.8%; Score 19.2; DB 6; Length 40304;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUUGCC 25
Db 37678 AACTTGAGGATCCAGATATTC 37655

RESULT 11
AA028866/c 2423 bp mRNA linear MAM 17-JUN-1999
LOCUS Bos taurus mRNA for prollyl oligopeptidase, complete cds.
DEFINITION Bos taurus mRNA for prollyl oligopeptidase, complete cds.
ACCESSION AA028866
VERSION AA028866.1 GI:5103284
KEYWORDS prollyl oligopeptidase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Cloning and expression of the cDNA encoding prollyl oligopeptidase
JOURNAL Biol. Pharm. Bull. 20 (10), 1047-1050 (1997)
MEDLINE 98014979
PUBMED 9353562
REFERENCE 2 (bases 1 to 2423)
AUTHORS Yoshimoto,T., Miyazaki,K., Haraguchi,N., Kitazono,A., Kabashima,T.
and Ito,K.
TITLE Direct Submission

```

JOURNAL Submitted (10-JUN-1999) Teutomu Kabashima, School of Pharmaceutical Sciences Nagasaki University, Department of Biotechnology; 1-14 Bunkyo-machi, Nagasaki, Nagasaki 852-8521, Japan (E-mail:t-kabashima@cc.nagasaki-u.ac.jp, Tel:81-95-847-1111(ex.2552), Fax:81-95-843-2444)

FEATURES Location/Qualifiers

source 1..2423 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_lib="brain" 120..2252 /EC_number="3.4.21.26" /codon_start=1 /product="prolyl oligopeptidase" /protein_id="BAA78907.1" /db_xref="GI:5103285" /translation="MLSFOYPDVYRDETAVDYHGHKICDPVAMLEDPSBOTKAFVE AONKITVPLEQCPIRGLYKEMTLDYDPKSCNFKKGYFYFYNTGLQNRVLVY QDSLEGEARVCLDPTSLDGTVALRGAFSEDEYVAYGLSASGSDWVTIKFMKVDG AKELADVLIRVKFSCMAWHDGKMFYNAIPQDGKSDGTETNLHQKLCYHVGITG QSEDIKCAEFDPDEPKWGGAEISDDGRYLLSIREGCDPVNRLWYCDLHQSPNGITGI LKWVKLIDNFEDEYDVYVNEGTVFTKTRHSPNRYLINIDFTDPEESRWLVPEHE KDVLWVACVPSNPLVLCYLDHDKNTLQLDHDMATGALLKTFPLEVGSVVGSGKKDT EIFQPTSPFLSPGIIYHCDLTKELEPRFREVTVKGDASDYQTVOIFPYSKDGTKI PMFIVHKKGIKLDGSHPAFLYGYGFNLSITPNYSVCKLIIFVRHMGVGLAVANIKGG EYGTWKKGGILANKQCFDDQCAAEYLIKEGYTSKRLTINGSGSGLLVATCANQ RPDIFGCVIAQGVMDMLKFHYTHIAWTTDYGCSNKHQFEMLIKTSPLHNVLKPE ADDIQPSMLLLTADHDDRVRVPLHSPKFIATLQLHVGSRKQNNPLLIHVDTKAGHGA GKPTAKVIEVSDMFAFARCLNDIWIQ"

ORIGIN

Query Match 76.8%; Score 19.2; DB 4; Length 2423; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0; QY 1 CAACUUCAGGAUUCAGAUUGCC 24 Db 956 CCACCTTCAGGATCCAGTGATGCC 933

RESULT 10 AX695905/c 40304 bp DNA linear PAT 31-MAR-2003 LOCUS AX695905 DEFINITION Sequence 1532 from Patent WO03008583. ACCESSION AX695905 VERSION AX695905.1 GI:29419070 KEYWORDS Homo sapiens (human) SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 AUTHORS Morris,D.W. and Engelhard,E.K. TITLE Novel compositions and methods for cancer JOURNAL Patent: WO 03008583-A 1532 30-JAN-2003; Sagres Discovery (US)

FEATURES Location/Qualifiers

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ORIGIN

Query Match 76.8%; Score 19.2; DB 6; Length 40304; Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0; QY 2 AACUUCAGGAUUCAGAUUGCC 25 Db 37678 AACTTGAGGATCCAGATATTC 37655


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repeat_region /note="AluX repeat: matches 1. .310 of consensus"
repeat_region 5677. .6268
repeat_region /note="LIME1 repeat: matches 5604. .6332 of consensus"
repeat_region 6302. .6481
repeat_region /note="L2 repeat: matches 2636. .2819 of consensus"
repeat_region complement(6483. .6755)
repeat_region /note="MERL15 repeat: matches 393. .688 of consensus"
repeat_region 6934. .6962
repeat_region /note="2.1 copies 14 mer TGCATGTATGTGCA 49% conserved"
repeat_region 6944. .6953
repeat_region /note="2.5 copies 4 mer TGCA 20% conserved"
repeat_region 6984. .7002
repeat_region /note="1.9 copies 10 mer TGCAGGTGTG 29% conserved"
repeat_region 6999. .7085
repeat_region /note="6.2 copies 14 mer GTGTATATGTACAT 66% conserved"
repeat_region 7000. .7014
repeat_region /note="2.5 copies 6 mer TGTACA 30% conserved"
repeat_region 7006. .7022
repeat_region /note="2.1 copies 8 mer TGTACATG 25% conserved"
repeat_region 7047. .7193
repeat_region /note="6.1 copies 24 mer GTGTGATGTGTATGTGCTGCG 113% conserved"
repeat_region 7048. .7080
repeat_region /note="5.5 copies 6 mer TGTGTA 30% conserved"
repeat_region 7053. .7085
repeat_region /note="4.1 copies 8 mer ATGTGTAT 29% conserved"
repeat_region 7118. .7127
repeat_region /note="2.5 copies 4 mer TGCA 20% conserved"
repeat_region 7125. .7136
repeat_region /note="2.0 copies 6 mer ATGTGT 24% conserved"
repeat_region 7148. .7164
repeat_region /note="2.8 copies 6 mer TGTGTA 25% conserved"
repeat_region 7203. .7332
repeat_region /note="L2 repeat: matches 3165. .3313 of consensus"
repeat_region 7333. .7342
repeat_region /note="2.5 copies 4 mer GAAT 20% conserved"
repeat_region 7347. .7532
repeat_region /note="MIR repeat: matches 2. .191 of consensus"
repeat_region complement(7537. .7640)
repeat_region /note="MIR repeat: matches 158. .262 of consensus"
repeat_region complement(8152. .8228)
repeat_region /note="MIR repeat: matches 184. .260 of consensus"
repeat_region 8253. .8341
repeat_region /note="L2 repeat: matches 3214. .3311 of consensus"
repeat_region 8504. .8516
repeat_region /note="2.6 copies 5 mer AGAGA 26% conserved"
repeat_region 8848. .8859
repeat_region /note="2.0 copies 6 mer AGTTCC 24% conserved"
repeat_region 9588. .9602
repeat_region /note="5.0 copies 3 mer GCA 21% conserved"
repeat_region 9920. .9935
repeat_region /note="2.0 copies 8 mer TTGGGGGG 32% conserved"
repeat_region 10303. .10313
repeat_region /note="2.2 copies 5 mer ACACA 22% conserved"
repeat_region 10428. .10439
repeat_region /note="3.0 copies 4 mer TGCT 24% conserved"
repeat_region 10570. .10580
repeat_region /note="2.2 copies 5 mer TTTC 22% conserved"
repeat_region complement(11386. .11858)
repeat_region /note="L2 repeat: matches 2722. .3312 of consensus"
gene 11913. .29288
gene /gene="NCF4"
mRNA join(11913. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29288)
gene /gene="NCF4"
/product="bkr83387.1 (neutrophil cytosolic factor 4
(40kD))"
/note="match: cDNAs: Em:AB002665 Em:X77094 Em:U59488
match: ESTs: Em:AA177839 Em:AI007048 Em:AA465462
Em:AA465389 Em:AA485518 Em:AI381940 Em:AA744805
```

```
Em:AA975113 Em:AA969460 Em:AA948430 Em:AI435296
Em:AI299103 Em:AA648472 Em:AA702857 Em:AI088359 Em:D20144
Em:AA299156 Em:AA688071 Em:W95229 Em:AI439568"
/evidence=not_experimental
complement(11982. .12109)
/note="L2 repeat: matches 2918. .3064 of consensus"
repeat_region 12358. .12367
repeat_region /note="3.3 copies 3 mer GGA 20% conserved"
repeat_region 12443. .12453
repeat_region /note="2.2 copies 5 mer GAGAC 22% conserved"
join(12542. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29193)
/gene="NCF4"
/note="match: proteins: Tr:O60808 Tr:P97369"
/codon_start=1
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Best Local Similarity 66.7%; Prid: No. 1.9e+02;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGAUCCAGAUUGCCC 25
Db 36754 AACTTGAGGATCCAGATATTTCCC 36731
||||:||||:||||:||||:||||:
AL390204 89566 bp DNA linear PRI 15-NOV-2001
Human DNA sequence from clone RP11-196D4 on chromosome 1, complete
sequence.
ACCESSION AL390204
VERSION AL390204.11 GI:16972946
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Smith.M.
Direct Submission
Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqu@sanger.ac.uk Clone requests: clones@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:16151421.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Swi,
SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WormPep
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-196D4 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-196D4 It may be shorter because we sequence overlapping
```

sections only once, except for a short overlap.

The true left end of clone RP11-196D4 is at 1 in this sequence. The true left end of clone RP11-307C12 is at 87567 in this sequence.

FEATURES

source
1. .89566
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-196D4"
/clone_lib="RPC1-11.1"

ORIGIN

Query Match 76.8%; Score 19.2; DB 9; Length 89566;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUUGCCC 25

|| : |||| : |||| : ||||

Db 74674 AATTCAGGATTCAGCTATGCC 74697

RESULT 14

AL672265.2/c

WPCOMMENT

Sequence split into 6 fragments LOCUS AL672265 Accession AL672265

Fragment Name Begin End

AL672265_0 1 110000

AL672265_1 100001 210000

AL672265_2 200001 310000

AL672265_3 300001 410000

AL672265_4 400001 510000

AL672265_5 500001 534015

Continuation (3 of 6) of AL672265 from base 200001 (AL672265 Homo sapiens chromosome 1)

Query Match

Best Local Similarity 76.8%; Score 19.2; DB 2; Length 110000;

Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUUGCCC 25

|| : |||| : |||| : ||||

Db 21515 AATTCAGGATTCAGCTATGCC 21492

RESULT 15

AP006116/c

LOCUS

AP006116 123325 bp DNA linear PLN 22-JUL-2003

DEFINITION Lotus corniculatus var. japonicus genomic DNA, chromosome 1,

clone:LjT40C04, TW0199, complete sequence.

ACCESSION AP006116

VERSION AP006116.1 GI:29122755

KEYWORDS HTG.

SOURCE

ORGANISM Lotus corniculatus var. japonicus (Lotus japonicus)

Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

REFERENCE

1

Authors Kaneko,T., Asamizu,E., Kato,T., Sato,S., Nakamura,Y. and Tabata,S.
Title Structural analysis of a Lotus japonicus genome. III. Sequence
features and mapping of sixty-two TAC clones which cover the 6.7 Mb
regions of the genome

Journal DNA Res. 10 (1), 27-33 (2003)

Medline 22579290

PubMed 12693552

REFERENCE

2

Authors Sato,S.

TITLE

Direct Submission
Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 232-0818, Japan (E-mail:bsato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 308.446 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	3 AAC64408	Aac64408 Human Nog
C 2	19.2	76.8	270	6 ABL70775	Ab170775 Corn tass
C 3	19.2	76.8	40304	9 ADA03014	Ada03014 Human NCF
C 4	19.2	76.8	40304	10 ADB72752	Adb72752 Human NCF
C 5	19.2	76.8	40304	10 ADC85494	Adc85494 Human Ncf
C 6	19.2	76.8	40304	12 ADM74609	Adm74609 Human car
C 7	19.2	76.8	86574	6 ABK83560	Abk83560 Human cDN
C 8	19.2	76.8	86574	13 ADR52822	Adr52822 Drug ther
9	18.6	74.4	391	8 ABX43504	Abx43504 Bovine ES
10	18.6	74.4	402	8 ABX45854	Abx45854 Bovine ES
11	18.6	74.4	422	8 ABX40707	Abx40707 Bovine ES
12	18.6	74.4	609	4 AAK86539	Aak86539 Human imm
C 13	18.6	74.4	110000	2 AAR42063	Continuation (11 o
C 14	18.4	73.6	8473	2 AAX25487	Aax25487 Human myo
C 15	18.2	72.8	2969	4 ABL02346	Ab102346 Drosophil
C 16	18.2	72.8	4530	4 ABL26458	Ab126458 Drosophil
C 17	17.6	70.4	460	9 ACH21863	Ach21863 Human adu
C 18	17.6	70.4	569	4 AAK94059	Aak94059 Human cDN
C 19	17.6	70.4	569	12 ADL30486	Adl30486 3' end of
20	17.6	70.4	576	4 AAK63128	Aak63128 Human imm

21	17.6	70.4	1362	4 ABL21915	Ab121915 Drosophil
22	17.6	70.4	1379	3 AAC59134	Aac59134 Human sec
23	17.6	70.4	1441	12 ADQ25167	Adq25167 Human sof
C 24	17.6	70.4	1994	4 AAI114791	Aai114791 Probe #47
C 25	17.6	70.4	1994	4 ABA56518	Aba56518 Human foe
C 26	17.6	70.4	1994	4 AAI36149	Aai36149 Probe #48
C 27	17.6	70.4	1994	4 ABA45986	Aba45986 Human bre
C 28	17.6	70.4	1994	4 ABA26148	Ab26148 Probe #46
C 29	17.6	70.4	1994	4 AAK30186	Aak30186 Human bon
C 30	17.6	70.4	1994	4 AAK04674	Aak04674 Human bra
C 31	17.6	70.4	1994	4 ABS29836	Abs29836 Human liv
C 32	17.6	70.4	1994	5 AAI04584	Aai04584 Probe #45
C 33	17.6	70.4	1994	6 ABS04773	Abs04773 Human gen
C 34	17.6	70.4	2130	2 AAK98543	Aak98543 Prolyl en
C 35	17.6	70.4	2562	8 ACC49473	Acc49473 Human pro
C 36	17.6	70.4	2562	10 ADE38352	Ade38352 Human pro
C 37	17.6	70.4	2562	13 ADR40162	Adr40162 Human pro
C 38	17.6	70.4	2712	10 ADB62183	Adb62183 Human cDN
C 39	17.6	70.4	2756	10 ADG89414	Adg89414 Cancer de
40	17.6	70.4	3362	4 ABL21914	Ab121914 Drosophil
41	17.6	70.4	3923	4 ABL21916	Ab121916 Drosophil
42	17.6	70.4	4744	4 AAS03072	Aas03072 Human dia
43	17.6	70.4	19696	4 AAL06639	Aal06639 Human rep
44	17.6	70.4	19696	5 AAS40722	Aas40722 DNA encod
45	17.6	70.4	19696	11 ADJ09928	Adj09928 Human pro

ALIGNMENTS

RESULT 1
AAC64408
ID AAC64408 standard; RNA; 25 BP.
XX AC AAC64408;
XX AC AAC64408;
DT 08-FEB-2001 (first entry)
XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4.
DE Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
KW stress-phosphorylated endoplasmic reticulum protein; cytoskeletal;
KW gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; antisense;
KW phosphorothioate; ss.
XX Homo sapiens.
XX Homo sapiens.

Key Location/Qualifiers
FT modified_base 1..25
FT /*tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.
PN 12-OCT-2000.
XX 07-APR-2000; 2000WO-US009383.
XX 08-APR-1999; 99US-0128372P.
XX 21-JUN-1999; 99US-0140331P.
XX (CHIR) CHIRON CORP.
XX Wei D, Halenbeck R, Williams LT;
XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides. The present sequence represents a human Nogo B

CC phosphorothioate antisense oligonucleotide from the present invention

XX

SQ Sequence 25 BP; 7 A; 8 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.046;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCCC 25

DB 1 CAACUUCAGGAUCCAGAUAGCCC 25

|||||

RESULT 2

ABL70775/c

ID ABL70775 standard; cDNA; 270 BP.

XX

AC ABL70775;

XX

DT 14-MAY-2002 (first entry)

XX

DE Corn tassal-derived polynucleotide (cdps) SEQ ID NO:149.

XX

XX Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPs;

KW inheritance; characteristic; growth; development; disease resistance;

KW environmental adaptability; quality; yield; molecular marker;

KW multigene trait; plant breeding; corn tassal; gene; ss.

XX

OS Zea mays.

XX

XX US2001051335-A1.

PN

XX

PD 13-DEC-2001.

XX

PF 16-APR-1999; 99US-00294093.

XX

XX 21-APR-1998; 98US-0082567P.

PR

XX (LALG/) LALGUDI R V.

PA (ITOL/) ITO L Y.

PA (SHER/) SHERMAN B K.

XX

XX Lalgudi RV, Ito LY, Sherman BK;

PI

XX WPI; 2002-163647/21.

DR

XX

PT Novel purified corn tassal-derived polynucleotide useful for determining

PT altered gene expression, to recover regulatory elements and to follow

PT inheritance of desirable characteristics through hybrid breeding

PT programs.

XX

PS Claim 1; SEQ ID NO 149; 201pp; English.

XX

XX The present sequence describes a purified corn tassal-derived

CC polynucleotide sequence (cdps) comprising a nucleic acid sequence

CC selected from those given in ABL70627 to ABL76833. The cdps sequences

CC encode corn tassal-derived polypeptides (CDPs). The cdps sequences (I)

CC can be used for determining altered gene expression, to recover

CC regulatory elements and to follow inheritance of desirable

CC

CC characteristics through hybrid breeding programs. (I) are also useful in

CC the evaluation, and alteration of desired characteristics associated with

CC growth and development, disease resistance, environmental adaptability,

CC quality and yield, and as molecular markers for studying inheritance of

CC multigene traits in a plant breeding program. (I) can be used to produce

CC a tassal-specific profile of gene transcription, a transcript image, to

CC clone regulatory elements for use in transformation vectors, to express a

CC polypeptide, to identify, isolate or extend identical or related corn

CC tassal nucleic acid sequences from DNA libraries, in nucleic acid

CC hybridisation or amplification technologies, as query sequences to

CC determine homology of known sequences, as probe for use in Southern or

CC Northern hybridisation, and to identify the presence of and/or to

CC determine the degree of similarity between two (or more) nucleic acid

CC sequences

XX

SQ Sequence 270 BP; 61 A; 46 C; 65 G; 98 T; 0 U; 0 Other;

Query Match 76.8%; Score 19.2; DB 6; Length 270;

Best Local Similarity 62.5%; Pred. No. 40;

Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCCC 25

DB 46 ATCTTCAGCATTCAGATATGACC 23

|||||

RESULT 3

ADA03014/c

ID ADA03014 standard; DNA; 40304 BP.

XX

AC ADA03014;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human NCF4 carcinoma associated gene, SEQ ID NO:1532.

XX

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;

KW gene; ds.

XX

OS Homo sapiens.

XX

XX WO2003057146-A2.

PN

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041414.

XX

XX 26-DEC-2001; 2001US-00035832.

PR

XX (SAGR-) SAGRES DISCOVERY.

XX

XX Morris DW;

PI

XX WPI; 2003-587068/55.

DR

XX

PT New recombinant nucleic acid encoding carcinoma associated protein,

PT useful for preparing compositions for treating carcinomas.

XX

PS Claim 1; SEQ ID NO 1532; 245pp; English.

XX

XX The invention relates to recombinant carcinoma associated (CA) nucleic

CC acid sequences from mouse and human (ADA01482-ADA03094), and to

CC recombinant carcinoma associated proteins (CAP) encoded by them. The

CC invention also encompasses expression vectors and host cells comprising a

CC CA nucleic acid, a polypeptide (especially an antibody) that specifically

CC binds to the protein, and a biochip comprising CA nucleic acid or

CC fragments thereof. The sequences of the invention were identified using

CC oncogenic retroviruses, which insert into the genome of the host organism

CC at random. Many of these do not carry transduced host oncogenes or

CC pathogenic trans-acting viral genes, meaning that cancer incidence is a

CC direct consequence of the effects of proviral integration into host

CC protooncogenes. The CA nucleic acid sequences can be used to diagnose

CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 9; Length 40304;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25

Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 4

ID ADB72752/c
ADB72752 standard; DNA; 40304 BP.

XX AC ADB72752;

DT 04-DEC-2003 (first entry)

XX DE Human NCF4 gene.

XX human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX OS Homo sapiens.

XX PN WO2003008583-A2.

XX PD 30-JAN-2003.

XX PF 26-DEC-2001; 2001WO-US051291.

XX PR 02-MAR-2001; 2001US-00798586.

XX PR 23-OCT-2001; 2001US-00004113.

XX PR 08-NOV-2001; 2001US-00032482.

XX PR 30-NOV-2001; 2001US-00997722.

XX PR 20-DEC-2001; 2001US-00034650.

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI Morris DW, Engelhard EK;

XX DR WPI; 2003-239337/23.

XX PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,

XX PT cancers, neoplasm, adenocarcinoma, or sarcomas.

XX PS Claim 1; SEQ ID NO 580; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a human gene of the invention.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 10; Length 40304;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25
Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 5

ID ADC85494/c
ADC85494 standard; DNA; 40304 BP.

XX AC ADC85494;

DT 01-JAN-2004 (first entry)

XX DE Human Ncf4 genomic sequence.

XX KW Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;

XX KW secreted; transmembrane; intracellular; ds.

XX OS Homo sapiens.

XX PN WO2003045230-A2.

XX PD 05-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038582.

XX PR 30-NOV-2001; 2001US-00997722.

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI Morris DW, Engelhard EK;

XX DR WPI; 2003-513603/48.

XX PT New recombinant nucleic acid comprising a nucleotide sequence of any of
PT the carcinoma-associated (CA) genes, useful for screening for drug
PT candidates for diagnosing or treating carcinomas.

XX PS Claim 1; SEQ ID NO 280; 983pp; English.

XX The invention relates to a recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the fully defined carcinoma-
CC associated (CA) genes from the 50 tables given in the specification. The
CC CA proteins are secreted, transmembrane or intracellular proteins. The
CC recombinant nucleic acids are useful for screening for drug candidates
CC for diagnosing or treating carcinomas. Sequences given in ADC85215-
CC ADC95514 represent CA genes of the invention.

XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;

Query Match 76.8%; Score 19.2; DB 10; Length 40304;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCC 25
Db 37678 AACTTGAGGATGCCAGATATTC 37655

RESULT 6

ID ADM74609/c
ADM74609 standard; DNA; 40304 BP.

XX AC ADM74609;

XX DT 01-JUL-2004 (first entry)

XX DE Human carcinoma associated (CA) nucleic acid #139.

XX KW Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
KW carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
KW cytostatic.

XX OS Homo sapiens.
XX PN US2004072154-A1.
XX PD 15-APR-2004.
XX XX 30-NOV-2001; 2001US-00997722.
XX PF 22-DEC-2000; 2000US-00747377.
XX PR 02-MAR-2001; 2001US-00798586.
XX XX (MORRIS/) MORRIS D W.
XX PA (ENGELHARD E K.
XX PI Morris DW, Engelhard EK;
XX XX WPI; 2004-328562/30.
XX PT New carcinoma associated gene or protein, useful for preparing a
PT composition for diagnosing or treating carcinoma e.g., leukemia or
PT lymphoma.
XX XX Claim 1; SEQ ID NO 280; 29pp; English.
XX XX The invention relates to new recombinant nucleic acids. The invention
CC also relates to a host cell comprising a recombinant nucleic acid or
CC expression vector, an expression vector comprising a recombinant nucleic
CC acid, a recombinant protein, a method of screening for drug candidates, a
CC method of screening for a bioactive agent capable of binding to a
CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
CC method of screening for a bioactive agent capable of modulating the
CC activity of a CAP, a method of evaluating the effect of a candidate
CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
CC the activity of a CAP, a method of treating carcinomas, a method of
CC neutralising the effect of a CAP and a method of diagnosing carcinoma or
CC propensity to carcinoma. A method of evaluating the effect of a candidate
CC carcinoma drug comprises administering the drug to a patient, removing a
CC cell sample from the patient and determining alterations in the
CC expression or activation of a gene comprising the nucleotide sequence. A
CC method of diagnosing carcinoma comprises determining the expression of
CC one or more genes comprising the nucleic acid sequence in a first tissue
CC type of a first individual and comparing the expression of the gene from
CC a second normal tissue type from the first individual or a second
CC unaffected individual, where a difference in the expression indicates
CC that the first individual has carcinoma. A method of inhibiting the
CC activity of a CAP comprises binding an inhibitor to the CAP. Treating
CC carcinomas comprises administering to a patient an inhibitor of CAP.
CC Neutralising the effect of a CAP comprises contacting an agent specific
CC for the CAP. The polypeptide specifically binds to the protein encoded by
CC the nucleic acid. It comprises an antibody that specifically binds to the
CC protein encoded by the nucleic acid. The nucleic acids are useful for
CC preparing a composition for diagnosing or treating carcinoma e.g.,
CC leukemia or lymphoma. This sequence represents a human carcinoma
CC associated (CA) nucleic acid of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX SQ Sequence 40304 BP; 9854 A; 9739 C; 9912 G; 10276 T; 0 U; 523 Other;
Query Match 76.8%; Score 19.2; DB 12; Length 40304;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 AACUUCAGGUAUCCAGUAUGCCC 25
|||: |||: |||: |||: |||: |||
Db 37678 AACUUCAGGUAUCCAGUAUATCCC 37655
RESULT 7
ABK83560/c
ID ABK83560 standard; cDNA; 86574 BP.

XX AC ABK83560;
XX DT 14-AUG-2002 (first entry)
XX DE Human cDNA differentially expressed in granulocytic cells #131.
XX XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX XX Homo sapiens.
OS WPI; 2002-435328/46.
XX PN WO200228999-A2.
XX PD 11-APR-2002.
XX XX 03-OCT-2001; 2001WO-US030821.
XX PF 03-OCT-2000; 2000US-0237189P.
XX PR (GENE-) GENE LOGIC INC.
XX PA Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
XX PI WPI; 2002-435328/46.
XX XX Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX PS Claim 1; SEQ ID NO 131; 114pp; English.
XX XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX	Sequence	86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;
XX	Query Match	76.8%; Score 19.2; DB 6; Length 86574;
XX	Best Local Similarity	66.7%; Pred. No. 91;
XX	Matches	16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY	2 AACUUCAGGAUCCAGAUAGCC 25	
DB	36754 AACCTGGAGGATCCAGATATCCC 36731	
AD	RESULT 8	
AD	ADR52822/c	
ID	ADR52822 standard; DNA; 86574 BP.	
XX	AC	
XX	ADR52822;	
XX	18-NOV-2004 (first entry)	
XX	Drug therapy altered expressed gene #173.	
DE		
XX		
XX	drug activity monitoring; expression profile; gene expression;	
KW	peripheral blood sample; peripheral blood mononuclear cell; drug therapy;	
KW	CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;	
KW	mTOR; ds.	
XX		
XX	Homo sapiens.	
OS		
XX	W02004072265-A2.	
PN		
XX	26-AUG-2004.	
PD		
XX	11-FEB-2004; 2004WO-US004118.	
XX		
XX	11-FEB-2003; 2003US-0446133P.	
PR	03-APR-2003; 2003US-0459782P.	
PR	23-JAN-2004; 2004US-0538246P.	
XX		
XX	(AMHP) WYETH.	
PA	(BURC/) BURCZYNSKI M.	
PA	(TWIN/) TWINE N.	
PA	(DORN/) DORNER A J.	
PA	(TREP/) TREPICCHIO W L.	
XX	Burczynski M, Twine N, Dornier AJ, Trepicchio WL;	
PI		
DR	WPI; 2004-642301/62.	
XX		
XX	Monitoring drug activities in vivo comprises comparing an expression	
PT	profile of a gene in a peripheral blood sample of a patient before and	
PT	after drug therapy.	
XX		
XX	Disclosure; SEQ ID NO 173; 136pp; English.	
XX		
CC	The invention relates to a method of monitoring drug activities in vivo	
CC	by comparing an expression profile of at least one gene in a peripheral	
CC	blood sample of a patient to a reference expression profile of the at	
CC	least one gene, where the at least one gene is differentially expressed	
CC	in peripheral blood mononuclear cells (PBMCs) of patients who have a non-	
CC	blood disease and are subjected to a drug therapy as compared to PBMCs	
CC	isolated from the patient before the drug therapy, and where the patient	
CC	has the non-blood disease and is being treated by the drug therapy. The	
CC	method, kit, and nucleic acid array are useful for monitoring drug	
CC	activities in vivo. The drug is especially CCI-779, an ester analogue of	
CC	the immunosuppressant rapamycin which is a potent inhibitor of the	
CC	mammalian target of rapamycin (mTOR). This sequence represents a gene	
CC	expressed in PBMC altered by the drug therapy. (Note: this sequence does	
CC	no form part of the printed specification but was obtained in electronic	
CC	format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).	
XX		
XX	Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 U; 0 Other;	

```
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 391 BP; 119 A; 76 C; 99 G; 97 T; 0 U; 0 Other;

Query Match      74.4%; Score 18.6; DB 8; Length 391;
Best Local Similarity 64.0%; Pred. No. 82;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCCC 25
   |||:::|||:||||:||||
Db 63 CAAATCTGGAGTCCAGATGCCCC 87

RESULT 10
ABX45854
ID ABX45854 standard; cDNA; 402 BP.
XX
AC ABX45854;
XX
DT 21-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #11019.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX
XX (MATH/) MATHIALAGAN N.
XX
XX (TAON/) TAO N.
XX
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 11019; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX complementary nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
```

```
CC CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 402 BP; 118 A; 76 C; 105 G; 103 T; 0 U; 0 Other;

Query Match      74.4%; Score 18.6; DB 8; Length 402;
Best Local Similarity 64.0%; Pred. No. 83;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCCC 25
   |||:::|||:||||:||||
Db 315 CAAATCTGGAGTCCAGATGCCCC 339

RESULT 11
ABX40707
ID ABX40707 standard; cDNA; 422 BP.
XX
AC ABX40707;
XX
DT 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #5872.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX
XX (MATH/) MATHIALAGAN N.
XX
XX (TAON/) TAO N.
XX
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 5872; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX complementary nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
```

CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The IMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=200201371139
XX
SQ Sequence 422 BP; 127 A; 79 C; 112 G; 102 T; 0 U; 2 Other;

Query Match 74.4%; Score 18.6; DB 8; Length 422;

Best Local Similarity 64.0%; Pred. No. 83;

Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCGAGUAGGCC 25

Db 252 CAAATTCGAGTCCAGATGTC 276

RESULT 12

AAK86539

ID AAK86539 standard; DNA; 609 BP.

XX AAK86539;

XX AAK86539;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41351.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

OS WO200157182-A2.

XX 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189974P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229503P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251031P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Baraash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 41351; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 609 BP; 152 A; 163 C; 172 G; 122 T; 0 U; 0 Other;
Query Match 74.4%; Score 18.6; DB 4; Length 609;
Best Local Similarity 72.0%; Pred. No. 88;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAACUUCAGGAUUCAGAUAGGCC 25
|||||:|||||:|||||:|||||

Db 566 CAACCTCAGGACTCCAGTCATGCCCC 590
RESULT 13
AAT42063_10/c
Continuation (11 of 19) of AAT42063 from base 1000001 (Haemophilus influenzae complete g
WP Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
WP Fragment Name Begin End
WP AAT42063_00 1 110000
WP AAT42063_01 100001 210000
WP AAT42063_02 200001 310000
WP AAT42063_03 300001 410000
WP AAT42063_04 400001 510000
WP AAT42063_05 500001 610000
WP AAT42063_06 600001 710000
WP AAT42063_07 700001 810000
WP AAT42063_08 800001 910000
WP AAT42063_09 900001 1010000
WP AAT42063_10 1000001 1110000
WP AAT42063_11 1100001 1210000
WP AAT42063_12 1200001 1310000
WP AAT42063_13 1300001 1410000
WP AAT42063_14 1400001 1510000
WP AAT42063_15 1500001 1610000
WP AAT42063_16 1600001 1710000
WP AAT42063_17 1700001 1810000
WP AAT42063_18 1800001 1830121
Query Match 74.4%; Score 18.6; DB 2; Length 110000;
Best Local Similarity 64.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAACUUCAGGAUUCAGAUAGGCC 25
|||||:|||||:|||||:|||||
Db 71778 CAACCTCAGGATGCCCTTTATGCC 71754
RESULT 14
AAK25487/c
ID AAK25487 standard; cDNA; 8473 BP.
XX
AC AAK25487;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human myosin IXa cDNA.
XX
KW Myosin IXa; human; Bardet-Biedl syndrome; Usher syndrome; diagnosis;
KW therapy; hearing loss; deafness; retinitis pigmentosa; obesity;
KW hypogonadism; sterility; polydactyly; brachydactyly; syndactyly;
KW mental retardation; renal abnormality; kidney disease; hypertension;
KW diabetes; cardiovascular abnormality; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 243..7889
FT /*tag= a /product= "myosin IXa"
FT
XX
XX WO9919489-A1.
XX
PD 22-APR-1999.
XX
PF 14-OCT-1998; 98WO-US021971.
XX
PR 15-OCT-1997; 97US-0062858P.
PR 17-OCT-1997; 97US-0062241P.
PR 30-DEC-1997; 97US-0068953P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Gorman SW, Welch J, Duhl D, Leng S, Adams A, Sheffield V;
PI

PI Chiu CY;
XX WPI; 1999-277643/23.
DR P-PSDB; AAY05781.
XX
XX Myosin Ixa and cyclic nucleotide gated channel-15 polypeptides.
XX
XX Claim 11; Fig 2; 69pp; English.
XX
XX This is the nucleotide sequence of human myosin Ixa cDNA. An isolated
CC nucleotide sequence comprising the present sequence, or nucleotides 243-
CC 7085, 243-680, 683-2399, 959-977, 2404-2747, 3158-3740 or 6473-6899, is
CC claimed. The cDNA was isolated from a human BAC contig that spanned
CC chromosomal region 15p22-23; the Bardet-Biedl syndrome gene maps to this
CC locus. Myosin Ixa is thus useful in the study, diagnosis and therapy of
CC Bardet-Biedl syndrome and Usher syndrome. The invention discloses myosin
CC Ixa and cyclic nucleotide gated channel-15 (CNGC-15) polypeptides,
CC polynucleotides, and compositions containing these polypeptides,
CC polynucleotides, expression cassettes, transformed cells and antibodies.
CC Conditions that can be treated by CNGC-15 and/or myosin Ixa polypeptides,
CC agonists and antagonists additionally include hearing loss, retinitis
CC pigmentosa, obesity, hypogonadism, sterility, polydactyly, brachydactyly,
CC syndactyly, mental retardation, renal abnormalities, hypertension,
CC diabetes and cardiovascular abnormalities (all claimed). Methods for the
CC expression and detection of CNGC-15 and myosin Ixa nucleotides and
CC polypeptides are also provided
XX
SQ Sequence 8473 BP; 2703 A; 1736 C; 1891 G; 2143 T; 0 U; 0 Other;
Query Match 73.6%; Score 18.4; DB 2; Length 8473;
Best Local Similarity 65.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
OY 2 AACUUCAGGAUUCAGAUAU 21
Db 1595 AACTTCAGGATTACAGATAT 1576
|||:||||:||||:||||:
|||:||||:||||:||||:
RESULT 15
ABL02346/c
ID ABL02346 standard; cDNA; 2969 BP.
XX
XX ABL02346;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 1520.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR P-PSDB; ABB58243.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX

PS Claim 1; SEQ ID NO 1520; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 2969 BP; 881 A; 625 C; 609 G; 854 T; 0 U; 0 Other;
Query Match 72.8%; Score 18.2; DB 4; Length 2969;
Best Local Similarity 65.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAACUUCAGGAUUCAGAUUGC 23
Db 425 CAACUUCAGGAUUCAGAUUGC 403
|||:||||:||||:||||:
|||:||||:||||:||||:
Search completed: July 30, 2005, 12:18:08
Job time : 311.446 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2561.15 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-4
Perfect score: 25
Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gse1:*
- 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
C 1	25	100.0	388	1	AA100508
C 2	23.4	93.6	823	2	BF694585
C 3	23.4	93.6	925	2	BF789989
C 4	21.8	87.2	216	2	BF229985
C 5	21.8	87.2	370	9	CG573906
C 6	21.8	87.2	380	9	CG539807
C 7	21.8	87.2	601	2	BF570751
C 8	21.8	87.2	739	2	BF693401
C 9	21.8	87.2	863	4	BI668593
C 10	20.8	83.2	432	1	AI225530
C 11	20.8	83.2	515	8	AZ513867
C 12	20.8	83.2	673	1	AV726731
C 13	20.8	83.2	698	2	BF791086
C 14	20.2	80.8	473	1	AA193133
C 15	20.2	80.8	587	2	BF687772
C 16	20.2	80.8	657	4	BG427535
C 17	20.2	80.8	687	6	CA163435
C 18	20.2	80.8	757	2	BF791087
C 19	20.2	80.8	826	4	BG426667
C 20	20.2	80.8	845	2	BF672700
C 21	19.2	76.8	314	2	BE845938
C 22	19.2	76.8	317	7	CN253955
C 23	19.2	76.8	342	6	CD706840
C 24	19.2	76.8	414	2	AW066689

25	19.2	76.8	427	8	AQ633324
C 26	19.2	76.8	433	4	BG349404
C 27	19.2	76.8	499	7	CK944021
C 28	19.2	76.8	513	4	BG349720
C 29	19.2	76.8	518	6	CB455616
C 30	19.2	76.8	630	7	CK979258
C 31	19.2	76.8	647	4	BG866086
C 32	19.2	76.8	732	9	CE807695
C 33	19.2	76.8	895	2	BF681266
C 34	19.2	76.8	1180	2	BF790177
C 35	18.8	75.2	522	2	AW642399
C 36	18.8	75.2	551	8	AQ321144
C 37	18.8	75.2	666	6	BY734522
C 38	18.8	75.2	700	1	AL508468
C 39	18.6	74.4	303	7	CR465805
C 40	18.6	74.4	316	6	CB708790
C 41	18.6	74.4	318	1	AA892501
C 42	18.6	74.4	408	2	BE328934
C 43	18.6	74.4	420	2	BF416636
C 44	18.6	74.4	439	1	AI717137
C 45	18.6	74.4	510	4	BI541804

ALIGNMENTS

RESULT 1
AA100508/c
LOCUS AA100508 388 bp mRNA linear EST 01-DEC-1996
DEFINITION zn51c07.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:561708 5' similar to TR:G307311 G307311 HISTONE H4. ;, mRNA sequence.
ACCESSION AA100508 GI:1646836
VERSION AA100508.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 388)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissos, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1132 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.
Location/Qualifiers
1. .388
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4594998"
/db_xref="taxon:9606"
/clone="IMAGE:561708"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene muscle 937209"

/note="Organ: skeletal muscle; Vector: pBluescript SK-; Site 1: ECORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'.

ORIGIN

Query Match 100.0%; Score 25; DB 1; Length 388;
Best Local Similarity 76.0%; Pred. No. 1;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25
||||:||||:||||:||||:||||:
Db 375 CAACTTCAGGATTCAGATATGCC 351

RESULT 2

BF694585/c
LOCUS 602081409F1 NIH_MGC_81 823 bp mRNA linear EST 22-DEC-2000
DEFINITION mRNA sequence.

ACCESSION BF694585
VERSION BF694585.1 GI:11979993
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 823)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI060 row: a column: 03

High quality sequence stop: 571.

FEATURES

source

1..823
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4245770"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_81"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 93.6%; Score 23.4; DB 2; Length 823;
Best Local Similarity 72.0%; Pred. No. 6.6;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25
||||:||||:||||:||||:||||:
Db 401 CAACTTCAGGATTCAGATATGCC 377

RESULT 3

BF789989/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4328127"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 93.6%; Score 23.4; DB 2; Length 925;
Best Local Similarity 72.0%; Pred. No. 6.7;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 25
||||:||||:||||:||||:||||:
Db 380 CAACTTCAGATTCAGATATGCC 356

RESULT 4

BF229985

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 216)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

BF789989 925 bp mRNA linear EST 12-JAN-2001
602249960F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4328127 5',
mRNA sequence.

ACCESSION BF789989

VERSION BF789989.1 GI:12095025

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 925)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI187 row: h column: 16

High quality sequence stop: 527.

FEATURES

source

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4328127"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

```

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. 370
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST206109"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

FEATURES
Source
Query Match 87.2%; Score 21.8; DB 9; Length 370;
Best Local Similarity 68.0%; Pred. No. 32;
Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCGAGUAUGCCC 25
|||||:::|||||:::|||||:::|||||

```

Db	136	CAACCTTCAGATTCCAAATATGCC	112
RESULT 6			
CG539807/c			
LOCUS			
DEFINITION			
CG539807			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			

screen to identify potential candidates for further characterization.
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

	source
1..380	Location/Qualifiers
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="129Sv/Ev"	
/db_xref="taxon:10090"	
/clone="OST131162"	
/cell_type="embryonic stem cell"	
/clone_lib="Mus musculus 129Sv/Ev"	

ORIGIN

Query Match	87.2%;	Score 21.8;	DB 9;	Length 380;
Best Local Similarity	68.0%;	Pred. No. 32;		
Matches 17;	Conservative	6;	Mismatches 2;	Indels 0;
0Y	1	CAACUUCAGGAUUCAGAUAGGCC	25	


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High quality sequence stop: 689.
Location/Qualifiers
1. .863
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5313024"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH MGC 96"
/notes="Organ: brain; Vector: pBluescriptR (modified
pluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH/MGC Library."

ORIGIN
Query Match 87.2%; Score 21.8; DB 4; Length 863;
Best Local Similarity 68.0%; Pred. No. 37;
Matches 17; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCGAGAUUGCC 25
||||| :|||:|:|:|:|:|
Db 405 CAACCTCAGAGTTCAGATATGCC 381

RESULT 10
AI225530/c
LOCUS
DEFINITION
u05b10.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1891003 5' similar to TR:Q63765 Q63765 RAT Cl-13 GENE
PRODUCT. ; mRNA sequence.
AI225530
AI225530.1 GI:3808583
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 432)
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
Waterston R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:975327
Seq primer: custom primer used
High quality sequence stop: 425.
Location/Qualifiers
1. .432
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1891003"
/sex="female"
/dev stage="adult"

FEATURES
source

/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/notes="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGG and 3' end
primer CGACCTGCGAGTCGAGCACA."

ORIGIN
Query Match 83.2%; Score 20.8; DB 1; Length 432;
Best Local Similarity 64.0%; Pred. No. 95;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCGAGAUUGCC 25
||||| :|||:|:|:|:|:|
Db 381 CACTTTCAGAAATTCGAATATGCC 357

RESULT 11
AI2513867/c
LOCUS
DEFINITION
IM0360008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M036008 F, genomic survey sequence.
AI2513867
AI2513867.1 GI:10695183
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 515)
Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,
Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,
Reilly M., Rose R., Stokes R., Tingey A., von
Niederhausern A. and Wright D., Weiss R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: J column: 08
Seg primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 515.
Location/Qualifiers
1. .515
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M036008"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 83.2%; Score 20.8; DB 8; Length 515;
Best Local Similarity 70.8%; Pred. No. 99;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 514 AACATCAGGATTCAGGTATGCC 491

RESULT 12

AV726731/c 673 bp mRNA linear EST 17-OCT-2000
LOCUS AV726731 HTC Homo sapiens cDNA clone HTCBNF02 5', mRNA sequence.
DEFINITION AV726731

VERSION AV726731.1 GI:10836152

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

Homo sapiens cDNA HTC clones

Unpublished (2000)

TITLE

Contact: Zeguag Han

JOURNAL

Chinese National Human Genome Center at Shanghai

COMMENT

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China

Tel: 86-21-50801919 (ex. 45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

1. .673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTCBNF02"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="HTC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 83.2%; Score 20.8; DB 1; Length 673;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 16; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 34 AACTTAAGATTCAGATATGCC 11

RESULT 13

LOCUS

BF791086/c

DEFINITION

698 bp mRNA linear EST 12-JAN-2001

602551165F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338353 5', mRNA sequence.

BF791086

BF791086.1 GI:12096140

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 698)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC1214 row: b column: 18

High quality sequence stop: 162.

FEATURES

source

1. .698
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4338353"
/lab_host="NIH MGC 81"
/clone_lib="NIH MGC 81"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 83.2%; Score 20.8; DB 2; Length 698;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 16; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUAGCCC 25

Db 110 AACTTCAGATTCAGATATGCC 87

RESULT 14

LOCUS

AA193133/c

DEFINITION

473 bp mRNA linear EST 12-MAR-1998

zq13c03.r1 Stratagene muscle 937209 Homo sapiens cDNA clone

IMAGE:629572 5' similar to TR:G307311 G307311 H1STONE H4. ; , mRNA sequence.

AA193133

AA193133.1 GI:1782528

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 473)


```

source
1. 587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4065893"
/tissue_type="Glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NHGMC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGAGCGCGGCAGCATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
```

ORIGIN

```

Query Match      80.8%; Score 20.2; DB 2; Length 587;
Best Local Similarity 68.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1  CAACUUCAGGAUUCGAGUAUGCCC 25
        |||::||| : ||||:|:|
Db      198 CAACCTTCAGATTCGCCAGATATGCC 174
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Search completed: July 30, 2005, 15:01:00
Job time : 2563.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:52:26 ; Search time 90.2027 Seconds
(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
 - 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq:*
 - 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.2	76.8	601	4	US-09-949-016-44986
C 2	19.2	76.8	601	4	US-09-949-016-44987
C 3	19.2	76.8	601	4	US-09-949-016-44988
C 4	19.2	76.8	165651	4	US-09-949-016-13032
C 5	18.8	75.2	237241	4	US-09-949-016-16101
C 6	18.6	74.4	1830121	4	US-09-557-884-1
C 7	18.6	74.4	1830121	4	US-09-643-990A-1
C 8	18.4	73.6	8473	3	US-09-172-422-2
C 9	17.4	69.6	66247	4	US-09-949-016-16009
C 10	17.4	69.6	128723	4	US-09-949-016-17533
C 11	17.2	68.8	15572	4	US-09-424-783-1
C 12	17.2	68.8	192700	4	US-09-949-016-11820
C 13	17.2	68.8	192704	4	US-09-949-016-17182
C 14	17	68.0	1742	4	US-09-205-258-9
C 15	17	68.0	38844	3	US-09-734-673-3
C 16	17	68.0	44393	4	US-09-949-016-14944
C 17	17	68.0	44393	4	US-09-949-016-14945
C 18	17	68.0	44393	4	US-09-949-016-14946
C 19	17	68.0	44393	4	US-09-949-016-16911
C 20	17	68.0	114793	4	US-10-148-806-3
C 21	17	68.0	524032	4	US-09-949-016-16928
C 22	17	68.0	524032	4	US-09-949-016-16929
C 23	17	68.0	524032	4	US-09-949-016-16930
C 24	17	68.0	524032	4	US-09-949-016-16931
C 25	17	68.0	529885	4	US-09-949-016-14340
C 26	17	68.0	529885	4	US-09-949-016-14341
C 27	17	68.0	529885	4	US-09-949-016-14342

C 28	17	68.0	529885	4	US-09-949-016-14343	Sequence 14343, A
C 29	17	68.0	529885	4	US-09-949-016-14344	Sequence 14344, A
C 30	17	68.0	529885	4	US-09-949-016-14345	Sequence 14345, A
C 31	17	68.0	529885	4	US-09-949-016-14346	Sequence 14346, A
C 32	17	68.0	529885	4	US-09-949-016-14347	Sequence 14347, A
C 33	16.8	67.2	465	4	US-09-640-211A-1911	Sequence 1911, Ap
C 34	16.8	67.2	954	4	US-09-328-352-3988	Sequence 3988, Ap
C 35	16.8	67.2	4305	4	US-09-645-593-1	Sequence 1, Appli
C 36	16.8	67.2	137949	4	US-09-949-016-12196	Sequence 12196, A
C 37	16.8	67.2	137956	4	US-09-949-016-17260	Sequence 17260, A
C 38	16.6	66.4	601	4	US-09-949-016-182462	Sequence 182462, A
C 39	16.6	66.4	601	4	US-09-949-016-182463	Sequence 182463, A
C 40	16.6	66.4	601	4	US-09-949-016-182464	Sequence 182464, A
C 41	16.6	66.4	601	4	US-09-949-016-182582	Sequence 182582, A
C 42	16.6	66.4	601	4	US-09-949-016-182583	Sequence 182583, A
C 43	16.6	66.4	601	4	US-09-949-016-182584	Sequence 182584, A
C 44	16.6	66.4	1651	4	US-09-270-767-29747	Sequence 29747, A
C 45	16.6	66.4	1761	4	US-09-270-767-13725	Sequence 13725, A

ALIGNMENTS

RESULT 1

US-09-949-016-44986/c
; Sequence 44986, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44986
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44986

Query Match 76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. NO. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTUCAGGATUCCAGAUAGCCC 25

Db 491 AATCCAGGATTCAGCTATGCC 469

RESULT 2

US-09-949-016-44987/c
; Sequence 44987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44987
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44987

Query Match          76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 368 AATTCAGGATTCAGCTATGCC 345

RESULT 3
US-09-949-016-44988/c
; Sequence 44988, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44988
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44988

Query Match          76.8%; Score 19.2; DB 4; Length 601;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 298 AATTCAGGATTCAGCTATGCC 275

RESULT 4
US-09-949-016-13032/c
; Sequence 13032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13032
; LENGTH: 165651

; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(165651)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13032

Query Match          76.8%; Score 19.2; DB 4; Length 165651;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCGAGAUAGCCC 25
   || : ||||| : ||||| : |||||
Db 13590 AATTCAGGATTCAGCTATGCC 13567

RESULT 5
US-09-949-016-16101/c
; Sequence 16101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16101
; LENGTH: 237241
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(237241)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16101

Query Match          75.2%; Score 18.8; DB 4; Length 237241;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCGAGAUAG 22
   ||||| : ||||| : ||||| : |||||
Db 189288 CAATTCAGGATTCAGGTATG 189267

RESULT 6
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
```

```

; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 74.4%; Score 18.6; DB 4; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 74;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUUGCCC 25
DB 1071778 CAACTTCAGGATGCCCTTTATGCC 1071754

RESULT 7
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover

```

```

; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 74.4%; Score 18.6; DB 4; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 74;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUUGCCC 25
DB 1071778 CAACTTCAGGATGCCCTTTATGCC 1071754

RESULT 8
US-09-172-422-2/c
; Sequence 2, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; CHANNEL-15 (CNCG-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172.422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-172-422-2

Query Match 73.6%; Score 18.4; DB 3; Length 8473;
Best Local Similarity 65.0%; Pred. No. 38;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACUUCAGAUUCCAGAUU 21
DB 1595 AACTTCAGGATTCAGATAT 1576

RESULT 9
US-09-949-016-16009/c
; Sequence 16009, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16009
; LENGTH: 66247
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16009

Query Match 69.6%; Score 17.4; DB 4; Length 66247;
Best Local Similarity 68.4%; Pred. No. 1.7e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 19
||||:||||:||||:
DB 60760 CAACTTAGGATCCAGAT 60742

RESULT 10
US-09-949-016-17533/c
; Sequence 17533, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17533
; LENGTH: 128723
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17533

Query Match 69.6%; Score 17.4; DB 4; Length 128723;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAU 20
||||:||||:||||:
DB 108647 AACTTCAGGATCCAGAA 108629

RESULT 11
US-09-424-783-1/c
; Sequence 1, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1

; LENGTH: 15572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-783-1

Query Match 68.8%; Score 17.2; DB 4; Length 15572;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 22
||||:||||:||||:
DB 13920 CAACTCCAGCTCCAGATG 13899

RESULT 12
US-09-949-016-11820
; Sequence 11820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11820
; LENGTH: 192700
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11820

Query Match 68.8%; Score 17.2; DB 4; Length 192700;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAU 22
||||:||||:||||:
DB 85389 CCATTTCAGGAATCCAGATG 85410

RESULT 13
US-09-949-016-17182
; Sequence 17182, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17182
; LENGTH: 192704
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17182

Query Match 68.8%; Score 17.2; DB 4; Length 192704;
 Best Local Similarity 63.8%; Pred. No. 2.5e+02;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACUCAGAGUCCAGAUAG 22
 DB 85389 CCATTTCAGGATCCAGATG 85410

RESULT 14
 US-09-205-258-49/c
 ; Sequence 49, Application US/09205258
 ; Patent No. 6325174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: P2007P1
 ; CURRENT APPLICATION NUMBER: US/09/205,258
 ; CURRENT FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,375
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,881
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,880
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,896
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,020
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,876
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,895
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,884
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,894
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,971
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,964
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,882
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,899
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,893
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,900
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,901
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,892
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,915
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,019
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,970
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,972
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,916
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,373
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,875
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,374
 ; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,917
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,949
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,974
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,883
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,897
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,898
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,962
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,963
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,877
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,878
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/070,923
 ; EARLIER FILING DATE: 1997-12-18
 ; EARLIER APPLICATION NUMBER: 60/092,921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/094,657
 ; EARLIER FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1227
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 49
 ; LENGTH: 1742
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (35)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURES:
 ; NAME/KEY: SITE
 ; LOCATION: (570)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-205-258-49
 Query Match 68.0%; Score 17; DB 4; Length 1742;
 Best Local Similarity 68.0%; Pred. No. 1.4e+02;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CAACUCAGAGUCCAGAUAGCCC 25
 DB 699 CAACUCAGAGUCCAGAUAGCCC 675
 RESULT 15
 US-09-734-675-3
 ; Sequence 3, Application US/09734675
 ; Patent No. 6365391
 ; GENERAL INFORMATION:
 ; APPLICANT: WEBSTER, Marion et al
 ; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CLO00862
 ; CURRENT APPLICATION NUMBER: US/09/734,675
 ; CURRENT FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 38844
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-734-675-3
 Query Match 68.0%; Score 17; DB 3; Length 38844;
 Best Local Similarity 64.0%; Pred. No. 2.4e+02;

Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAACTUCAGGAUUCGAGAUUGGCC 25
|||: || |:| ||| |:| |||
Db 14970 CAACTACAAAATTCTAGAAATGCC 14994

Search completed: July 30, 2005, 15:05:43
Job time : 98.2027 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	24	100.0	144	6	CQ688348	Sequence
C 2	24	100.0	170	6	CQ712889	Sequence
C 3	24	100.0	191	6	CQ683936	Sequence
C 4	24	100.0	207	11	G05614	human STS
C 5	24	100.0	370	6	CQ709205	Sequence
C 6	24	100.0	468	6	CQ686446	Sequence
C 7	24	100.0	496	6	AX895341	Sequence
C 8	24	100.0	496	6	BD030874	Sequence
C 9	24	100.0	536	6	CQ781164	Sequence
C 10	24	100.0	536	6	BD125873	Primer for
C 11	24	100.0	559	6	CQ782338	Sequence
C 12	24	100.0	559	6	BD127047	Primer for
C 13	24	100.0	1079	9	BC007109	Homo sapi
C 14	24	100.0	1206	9	AK172726	Homo sapi
C 15	24	100.0	1213	6	BD194907	86 human
C 16	24	100.0	1213	6	CQ855235	Sequence
C 17	24	100.0	1466	9	BC071848	Homo sapi
C 18	24	100.0	1610	6	BD231889	Bone marr
C 19	24	100.0	1617	9	AF087901	Homo sapi

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. Liew, C.C., Marshall, W.E. and Zhang, H.
 Compositions and methods relating to osteoarthritis
 Patent: WO 02070737-A 57815 12-SEP-2002;
 Chondrogene Inc. (CA)

FEATURES

source
 1. .170
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 170;
 Best Local Similarity 79.2%; Pred. No. 3.5;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 97 ATTCACCAGTGCTCAGATAGGA 74

RESULT 3

CQ683836/c
 LOCUS CQ683836 191 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 28762 from Patent WO02070737.
 ACCESSION CQ683836
 VERSION CQ683836.1 GI:42207284

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. Liew, C.C., Marshall, W.E. and Zhang, H.

Compositions and methods relating to osteoarthritis

Patent: WO 02070737-A 28762 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

source

1. .191

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 191;
 Best Local Similarity 79.2%; Pred. No. 3.4;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 116 ATTCACCAGTGCTCAGATAGGA 93

RESULT 4

G05614
 LOCUS G05614 207 bp DNA linear STS 19-OCT-1995
 DEFINITION human STS WI-6613, sequence tagged site.
 ACCESSION G05614

VERSION G05614.1 GI:858859

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 207)

Hudson, I.

Whitehead Institute/MIT Center for Genome Research; Physically

Mapped ESTs

Unpublished (1995)

COMMENT

Contact: Thomas Hudson

Whitehead Institute/MIT Center for Genome Research

Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: TAGCTTCACCATCTCTGCAA

Primer B: GTCTTGACTGCATGTGTCA

STS size: 175

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Tag Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Prepared with primer pairs derived from Z38593 -- dbEST.

FEATURES

source

Location/Qualifiers

1. .207

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="743 G.4; 758 E.5; 919 A.6; 919 F.3; 909 E.11; 222.4

cr from top of Chr2 linkage group"

STS

primer_bind

2. .176

complement(156. .176)

ORIGIN

Query Match 100.0%; Score 24; DB 11; Length 207;

Best Local Similarity 79.2%; Pred. No. 3.3;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACCAGGCGCUCAGAUAGGA 24

Db 76 ATTCACCAGTGCTCAGATAGGA 99

RESULT 5

CQ709205/c

LOCUS CQ709205 370 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 54131 from Patent WO02070737.

ACCESSION CQ709205

VERSION CQ709205.1 GI:42270021

KEYWORDS

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. Liew, C.C., Marshall, W.E. and Zhang, H.

Compositions and methods relating to osteoarthritis

Patent: WO 02070737-A 54131 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

source

Location/Qualifiers

1. .370

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 536;
Best Local Similarity 79.2%; Pred. No. 2.8;


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DEFINITION Homo sapiens reticulon 4, transcript variant 3, mRNA (cdna clone
IMAGE:4291127), complete cds.
ACCESSION BC007109.1 GI:13937989
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scapleton, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Carninci, P., Prange, C., Kaha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
PROC. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL
PUBMED 2 (bases 1 to 1079)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 21 Row: h Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: The cds is short compared to
the longest cds in the locus.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4291127"
/tissue_type="Skeletal Muscle"
/clone_lib="NIH_MGC_81"
/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
1. .1079
/gene="RTN4"
/notes="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"
gene
FEATURES
source
1. .1079
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
1. .1079
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DEFINITION Homo sapiens reticulon 4, isoform C"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
112. .711
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/product="reticulon 4, isoform C"
/protein_id="AAH07109.1"
/db_xref="GI:13937990"
/db_xref="LocusID:57142"
/db_xref="MIM:604475"
/translation="MDGQKNWKDKVVDLLYRDKTKTGVVFGASFLLLSLTVFSTV
SVTAYTALALLSVTISFRLYKGVIOAIQKSDGHPRAVLESEVAISEELVOKYSNSA
LGHVNTIIEKLRLFLVDDLVSLKFAVLAWFTYVGCALFNGTLILILILISLFSVPV
IYERHQADIDHYGLANKVKNVQKMAKIQAKIPGLKRRKAE"
ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1079;
Best Local Similarity 79.2%; Pred. No. 2.4;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACGAGUGCCUCAGAUAGGA 24
Db 976 ATTCACCACTGCTCAGATAGGA 953
RESULT 14
AKI72726/c
LOCUS AKI72726 1206 bp mRNA linear PRI 11-MAY-2004
DEFINITION Homo sapiens cDNA PSC0023 fis, clone: NT2RP1000386.
ACCESSION AKI72726
VERSION AKI72726.1 GI:47115505
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,
Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.
HRI human cDNA sequencing project
Unpublished
2 (bases 1 to 1206)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (20-APR-2004) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
292-0818, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975,
Fax:81-438-52-3986)
COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
Location/Qualifiers
1. .1206
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP1000386"
/cell_line="NT2"
/clone_lib="NT2RP1"
/notes="cloning vector: pUC19FL3-mRNA from NT2 neuronal
precursor cells after 48-hours retinoic acid (RA)
induction."
ORIGIN
Query Match 100.0%; Score 24; DB 9; Length 1206;
Best Local Similarity 79.2%; Pred. No. 2.4;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACGAGUGCCUCAGAUAGGA 24

```

Search completed: July 30, 2005, 12:54:29
Job time : 703.486 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 10:32:26 ; Search time 296.108 Seconds
(without alignments)
479.804 Million cell updates/sec

Title: US-09-544-776-5
Perfect score: 24
Sequence: 1 auuccaccagucucagauagga 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	3 AAC64409	Aac64409 Human Nog
2	24	100.0	496	3 AAC07129	Aac07129 Human sec
3	24	100.0	536	4 AAK92844	Aak92844 Human CDN
4	24	100.0	536	12 ADL29271	Adl29271 3' end of
5	24	100.0	559	4 AAK94018	Aak94018 Human CDN
6	24	100.0	559	12 ADL30445	Adl30445 3' end of
7	24	100.0	972	10 ADG63407	Adg63407 Partial h
8	24	100.0	1213	2 AAX04379	Aax04379 Human sec
9	24	100.0	1610	3 AAZ36230	Aaz36230 cDNA enco
10	24	100.0	1683	4 AAD08386	Aad08386 Human sec
11	24	100.0	1694	4 AAK94408	Aak94408 Human ful
12	24	100.0	1694	12 ADL31137	Adl31137 Full leng
13	24	100.0	1758	4 AAF32725	Aaf32725 Human sec
14	24	100.0	1785	12 ADKL4166	Adkl4166 Human aut
15	24	100.0	2235	6 ABV94681	Abv94681 Human pan
16	24	100.0	2240	3 AAC64406	Aac64406 Human Nog
17	24	100.0	2386	2 AAV30920	Aav30920 Human sec
18	24	100.0	2386	5 AAF98399	Aaf98399 Human CDN
19	24	100.0	2512	12 ADQ15813	Adq15813 4 synthes
20	24	100.0	3919	12 ADP45550	Adp45550 Human Nog

C	21	24	100.0	4053	4 AAS09453	Aas09453 Human CDN
C	22	24	100.0	4053	9 ACC81048	Acc81048 Human Nog
C	23	24	100.0	4053	12 ADP13574	Adp13574 Renal cel
C	24	24	100.0	4093	3 AAA23454	Aaa23454 cDNA enco
C	25	24	100.0	4632	6 ABV94680	Abv94680 Human pan
C	26	24	100.0	4632	10 ADG32772	Adg32772 Human DNA
C	27	24	100.0	4698	8 ABX34563	Abx34563 Human mdd
C	28	24	100.0	4710	4 AAL04697	Aal04697 Human rep
C	29	24	100.0	4710	4 ABL97604	AbL97604 Human tes
C	30	24	100.0	4789	13 ADR83534	Adr83534 Human ret
C	31	24	100.0	4822	6 ABS70449	Abs70449 Human bon
C	32	22	91.7	25	12 ADP17627	Adp17627 Renal cel
C	33	22	91.7	211	2 AAX23499	Aax23499 Human neu
C	34	22	91.7	360	5 AAS29079	Aas29079 cDNA enco
C	35	22	91.7	360	6 ABS68219	Abs68219 cDNA enco
C	36	22	91.7	360	10 ADC25213	Adc25213 Human CDN
C	37	22	91.7	377	5 AAS29151	Aas29151 cDNA enco
C	38	22	91.7	377	6 ABS68291	Abs68291 cDNA enco
C	39	22	91.7	377	10 ADC25285	Adc25285 Human CDN
C	40	22	91.7	385	4 AAH72193	Aah72193 Human cer
C	41	22	91.7	410	9 ACH35051	Ach35051 Human end
C	42	22	91.7	510	4 AAH69329	Aah69329 Human cer
C	43	22	91.7	602	5 ABV49730	Abv49730 Human pro
C	44	22	91.7	633	5 ABV19969	Abv19969 Human pro
C	45	22	91.7	702	4 AAH71132	Aah71132 Human cer

ALIGNMENTS

RESULT 1
AAC64409
ID AAC64409 standard; RNA; 24 BP.

XX AAC64409;

DT 08-FEB-2001 (first entry)

XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:5.

XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
XX stress-phosphorylated endoplasmic reticulum protein; cytosol; brain tumour;
XX gene therapy; cell growth; cellular stress response; neuron growth;
XX regulator of oxidative stress; inhibitor of neurite outgrowth;
XX axon regeneration; diagnosis; cancer; identification; antisense;
XX phosphorothioate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH modified_base 1..24
FT /tag= a
FT /note= "phosphorothioate linkages"

XX WC0200060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating stress levels, cell growth, diagnosis and treatment of cancer and malignant growth and for identifying agonists and antagonists.

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can: regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides. The present sequence represents a human Nogo B

CC phosphorothioate antisense oligonucleotide from the present invention

XX

SQ Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.12; Length 24;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|||||

Db 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|||||

RESULT 2

ID AAC07129/c

XX AAC07129 standard; cDNA; 496 BP.

AC AAC07129;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 11204.

XX

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

XX

OS Homo sapiens.

XX

PI EP1033401-A2.

XX

XX 06-SEP-2000.

XX

XX 21-FEB-2000; 2000EP-00200610.

XX

XX 26-FEB-1999; 99US-0122487P.

XX

PA (GEST) GENSET.

XX

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX

XX WPI; 2000-500381/45.

XX

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX

XX Claim 1; SEQ ID NO 11204; 71pp + Sequence Listing; English.

XX

XX The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'

CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in

CC

CC diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors

XX

SQ Sequence 496 BP; 156 A; 77 C; 104 G; 158 T; 0 U; 1 Other;

Query Match 100.0%; Score 24; DB 3; Length 496;

Best Local Similarity 79.2%; Pred. No. 0.19;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|:|||||:|||||:|||||

Db 410 ATTCCACCAGTGCCTCAGATAGGA 387
|:|||||:|||||:|||||

RESULT 3

AAK92844

ID AAK92844 standard; cDNA; 536 BP.

XX

AC AAK92844;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human cDNA 3'-end sequence, SEQ ID NO: 1304.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PI EP1130094-A2.

XX

XX 05-SEP-2001.

XX

XX 07-JUL-2000; 2000EP-00114089.

XX

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

XX WPI; 2001-524255/58.

XX

XX 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

XX

XX Claim 3; SEQ ID NO 1304; 1380pp + Sequence Listing; English.

XX

XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been isolated

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full

CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special

CC methods. The present sequence is the nucleotide sequence of the 3'-end of

CC a cDNA provided in the invention. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in CD-

CC ROM format directly from EPO

XX

SQ Sequence 536 BP; 169 A; 120 C; 92 G; 148 T; 0 U; 7 Other;

Query Match 100.0%; Score 24; DB 4; Length 536;

Best Local Similarity 79.2%; Pred. No. 0.2;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AUUCCACCAGUGCCUCAGAUAGGA 24
|:|||||:|||||:|||||

Db 76 ATTCCACCAGTGCCTCAGATAGGA 99
|:|||||:|||||:|||||


```

OS Homo sapiens.
XX
XX PN EP1130094-A2.
XX
XX PD 05-SEP-2001.
XX
XX PF 07-JUL-2000; 2000EP-00114089.
XX
XX PR 08-JUL-1999; 99JP-00194486.
XX
XX PR 11-JAN-2000; 2000JP-00118774.
XX
XX PR 02-MAY-2000; 2000JP-00183765.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otauki T, Koga H;
XX
XX DR WPI; 2001-524255/58.
XX
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX
XX PS Example 11; SEQ ID NO 2478; 1380pp + Sequence Listing; English.
XX
XX CC The invention relates to primers for synthesising full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesising the full length cDNA are useful
XX CC for clarifying the function of the protein encoded by the cDNA. The full
XX CC length clones were obtained by construction of full length enriched cDNA
XX CC libraries that were synthesised by the oligo-capping method. The primers
XX CC enable the production of the full length cDNA easily without any special
XX CC methods. The present sequence was used as the representative sequence
XX CC from a human clone which was used in homology searches to identify the
XX CC clone. Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in CD-ROM format directly from
XX CC EPO
XX
XX SQ Sequence 559 BP; 178 A; 129 C; 94 G; 152 T; 0 U; 6 Other;

Query Match 100.0%; Score 24; DB 4; Length 559;
Best Local Similarity 79.2%; Pred. NO. 0.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATUCCACCAGUGCCUCAGAUAGGA 24
Db |:|||||:|||||:|||||:
76 ATTCACCAAGTCCTCAGATAGGA 99

RESULT 6
ADL30445
ID ADL30445 standard; cDNA; 559 BP.
XX
XX AC ADL30445;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE 3' end of a representative human cDNA cluster SeqID 2478.
XX
XX KW human; medicine; signal transduction; glycoprotein; transcription;
XX KW oligo-capping method; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1396543-A2.
XX
XX PD 10-MAR-2004.
XX
XX PF 07-JUL-2000; 2003EP-00025638.
XX
XX PR 08-JUL-1999; 99JP-00194486.
XX
XX PR 11-JAN-2000; 2000JP-00118774.
XX
XX PR 02-MAY-2000; 2000JP-00183865.

```

```

PR 07-JUL-2000; 2000EP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX length human cDNAs.
XX
XX Example 18; SEQ ID NO 2478; 1340pp; English.
XX
XX This invention relates to a novel primers useful for synthesising full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction.
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is the
XX 3' end of a representative human DNA cluster of the invention.
XX
XX Sequence 559 BP; 178 A; 129 C; 94 G; 152 T; 0 U; 6 Other;
SQ

```

Query Match 100.0%; Score 24; DB 12; Length 559;
Best Local Similarity 79.2%; Pred. No. 0.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 76 ATCCACCAGTGCCTCAGATAGGA 99

```

RESULT 7
ADG63407/c
ID ADG63407 standard; cDNA; 972 BP.
XX
XX ADG63407;
XX
XX 11-MAR-2004 (first entry)
XX Partial human Nogo cDNA.
XX
XX ss; human; neuropsychiatric disorder; Nogo polymorphism; Nogo;
XX polymorphism; schizophrenia.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(244..249,ct)
XX /*tag= a
XX /note= "Deletion associated with CAA polymorphism"
XX variation replace(725..729,cc)
XX /*tag= b
XX /note= "Polymorphism"
XX
XX US2003215868-A1.
XX
XX 20-NOV-2003.
XX
XX 15-MAY-2003; 2003US-00437931.
XX
XX 16-MAY-2002; 2002GB-00011212.
XX
XX (SEEM/) SEEMAN P.
XX (NOVA/) NOVAK G.
XX (TALL/) TALLERICO T.
XX
XX Seeman P, Novak G, Tallerico T;
XX
XX WPI; 2003-902032/82.
XX

Determining susceptibility of patient to neuropsychiatric disorder, by obtaining sample from patient, and testing the sample for presence of polymorphism in Nogo gene.

Claim 2; SEQ ID NO 1; 12pp; English.

The invention relates to a method of determining the susceptibility of a patient to a neuropsychiatric disorder, comprising obtaining a sample from a patient, and testing the sample for the presence of a polymorphism in the Nogo gene, where the presence of a polymorphism indicates that the patient is susceptible to a neuropsychiatric disorder. The method is useful for determining the susceptibility of a patient to a neuropsychiatric disorder e.g. schizophrenia. The present sequence represents human Nogo partial cDNA.

Sequence 972 BP; 326 A; 155 C; 178 G; 313 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 10; Length 972;
Best Local Similarity 79.2%; Pred. No. 0.22;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
   |:|||||:|||||:|||||:|||||
DB 265 ATCCACCAGTGCCTCAGATAGGA 242

```

RESULT 8
AAAX04379/c
ID AAAX04379 standard; DNA; 1213 BP.
XX
XX AAAX04379;
XX
XX 13-APR-1999 (first entry)
XX Human secreted protein gene 69 clone HAGFT48.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
XX
XX WO9856804-A1.
XX
XX 17-DEC-1998.
XX
XX 11-JUN-1998; 98WO-US012125.
XX
XX 13-JUN-1997; 97US-0049547P.
XX 13-JUN-1997; 97US-0049548P.
XX 13-JUN-1997; 97US-0049549P.
XX 13-JUN-1997; 97US-0049550P.
XX 13-JUN-1997; 97US-0049566P.
XX 13-JUN-1997; 97US-0049606P.
XX 13-JUN-1997; 97US-0049607P.
XX 13-JUN-1997; 97US-0049608P.
XX 13-JUN-1997; 97US-0049609P.
XX 13-JUN-1997; 97US-0049610P.
XX 13-JUN-1997; 97US-0049611P.
XX 13-JUN-1997; 97US-0050901P.
XX 08-JUL-1997; 97US-0052989P.
XX 18-AUG-1997; 97US-0051919P.
XX 12-SEP-1997; 97US-0055984P.
XX 12-SEP-1997; 97US-0058665P.
XX 12-SEP-1997; 97US-0058668P.
XX 12-SEP-1997; 97US-0058669P.
XX 12-SEP-1997; 97US-0058750P.

XX Human secreted protein-encoding gene 42 cDNA clone HAGT48, SEQ ID NO:52.
DE
XX Human; secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angioinfectious disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulvectomy; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification;
KW ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 830..1192
FT /*tag= a
FT /product= "Human secreted protein precursor"
FT /note= "CDS does not include start codon"
FT /partial
FT sig_peptide 830..898
FT /*tag= b
FT mat_peptide 899..1189
FT /*tag= c
FT /product= "Mature human secreted protein"
XX
XX WO200077022-A1.
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US015136.
XX
XX 11-JUN-1999; 99US-0138629P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI, 2001-367020/38.
XX P-PSDB; AAE03939.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX disease, botulism, cancers and Scimitar syndrome.
XX
XX Claim 1; Page 520; 614pp; English.
XX
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.
XX The genes and their secreted proteins are useful for preventing, treating
XX or ameliorating medical conditions, e.g. by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 50 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angioinfectious disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
XX invention
SQ Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
Query Match 100.0%; Score 24; DB 4; Length 1683;
Best Local Similarity 79.2%; Pred. NO. 0.23;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATCCACCCAGGCGCCAGCAUAGGA 24
Db 1549 ATTCCACCATGCTCAGATAGGA 1526
RESULT 11
AAK94408/c
ID AAK94408 standard; cDNA; 1694 BP.
XX
AC AAK94408;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 3170.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
EN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Negai K, Kojima S, Otsuki T, Koga H;
DR WPI; 2001-524255/58.
DR P-PSDB; AAM93484.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
PS Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesising the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a full length human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in CD-ROM format directly
XX from EPO
XX
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 4; Length 1694;
Best Local Similarity 79.2%; Pred. NO. 0.23;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGUCUCAGAUAGGA 24
 Db 1619 ATTCACACGAGGCTCAGATAGGA 1596

RESULT 12
 ADL31137/c
 ID ADL31137 standard; cDNA, 1694 BP.
 AC ADL31137;
 DT 20-MAY-2004 (first entry)
 XX Full length human cDNA clone SeqID 3170.
 DE human; medicine; signal transduction; glycoprotein; transcription;
 KW oligo-capping method; ss; gene.
 KW Homo sapiens.
 OS EPI396543-A2.
 PN 10-MAR-2004.
 XX 07-JUL-2000; 2003EP-00025638.
 XX 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2004-204755/20.
 DR P-PSDB; ADL31138.
 XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 XX Example 1; SEQ ID NO 3170; 1340pp; English.
 XX This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3',
 CC ends using the oligo-capping method. This polynucleotide sequence is a
 CC full length human cDNA clone of the invention.
 XX Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 24; DB 12; Length 1694;
 Best Local Similarity 79.2%; Pred. No. 0.23;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGUCUCAGAUAGGA 24
 Db 1619 ATTCACACGAGGCTCAGATAGGA 1596

RESULT 13
 AAF32725
 ID AAF32725 standard; cDNA, 1758 BP.
 XX AAF32725;
 AC AAF32725;
 XX 23-MAR-2001 (first entry)

XX Human secreted protein gene 27 SEQ ID NO:37.
 DE Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
 KW ocular disorder; corneal infection; wound healing; food additive;
 KW preservative; ss.
 XX Homo sapiens.
 OS WO200077255-A1.
 PN 21-DEC-2000.
 PD 01-JUN-2000; 2000WO-US014926.
 XX 11-JUN-1999; 99US-0138628P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM, Komatsoulis GA;
 PI WPI; 2001-025337/03.
 DR P-PSDB; AAB64448.
 XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX Claim 1; Page 495; 593pp; English.
 PS The polynucleotide sequences given in AAF32699 to AAF32747 encode the
 CC human secreted proteins given in AAB64422 to AAB64470. AAB64471 to
 CC AAB64548 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;
 CC ophthalmological. The polynucleotides and polypeptides can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities. AAF32690 to AAF32698 and
 CC AAB64421 represent sequences used in the exemplification of the present
 CC invention
 XX Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;
 SQ Query Match 100.0%; Score 24; DB 4; Length 1758;
 Best Local Similarity 79.2%; Pred. No. 0.24;
 Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGGUCUCAGAUAGGA 24
 Db 746 ATTCACACGAGGCTCAGATAGGA 769

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 11:50:11 ; Search time 2458.7 Seconds
(without alignments)
371.555 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 aauccaccaguccuagaggga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	125	1	AI216602
2	24	100.0	127	4	BM725018
3	24	100.0	174	2	BE620536
C 4	24	100.0	176	7	T30356
C 5	24	100.0	179	5	BU963350
C 6	24	100.0	195	4	BG271724
C 7	24	100.0	196	7	F00105
8	24	100.0	207	7	Z38593
C 9	24	100.0	209	1	AA252742
C 10	24	100.0	237	1	AA989076
C 11	24	100.0	245	2	AW148462
12	24	100.0	247	1	AI796628
13	24	100.0	258	7	T82303
14	24	100.0	262	6	CD368992
C 15	24	100.0	267	2	BF734642
C 16	24	100.0	281	4	BG170953
17	24	100.0	287	7	F10097
18	24	100.0	287	7	F10120
19	24	100.0	287	7	T54784
20	24	100.0	289	7	T33248
21	24	100.0	290	1	AA176619
C 22	24	100.0	295	4	BG121948
C 23	24	100.0	301	1	AA306723
C 24	24	100.0	305	7	W46607

C 25	24	100.0	312	1	AA236753
26	24	100.0	321	2	AW468088
27	24	100.0	322	1	AI874377
C 28	24	100.0	341	1	AA236111
29	24	100.0	347	7	T34689
30	24	100.0	350	1	AI279315
31	24	100.0	351	5	BU681625
C 32	24	100.0	352	7	T31420
C 33	24	100.0	353	1	AV708414
C 34	24	100.0	354	4	BM452395
C 35	24	100.0	355	2	BE172028
36	24	100.0	365	1	AA084644
37	24	100.0	379	1	AA159037
C 38	24	100.0	382	1	AV682540
C 39	24	100.0	386	4	BM721543
40	24	100.0	386	7	N22319
C 41	24	100.0	390	1	AV648293
42	24	100.0	396	1	AI367513
C 43	24	100.0	396	1	AV648219
C 44	24	100.0	397	7	W37994
C 45	24	100.0	400	1	AA235659

ALIGNMENTS

RESULT 1	AI216602	125 bp	mRNA	linear	EST 02-DEC-1998
LOCUS	qm33a05.xl	NCI_CGAP_Lu5	Homo sapiens	cdna	clone IMAGE:1883600 3',
DEFINITION	mRNA sequence.				
ACCESSION	AI216602				
VERSION	AI216602.1	GI:3785643			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 125)				
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 965 Std Error: 0.00 Seq primer: -40UP from Gibco.				
FEATURES	Location/Qualifiers				
source	1..125				
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	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:1883600"				
	/tissue_type="carcinoid"				
	/lab_host="DH10B"				
	/clone_lib="NCI CGAP Lu5"				
	/note="Organ: lung; Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Ronaldo."				
ORIGIN					

Bult, C.J., Lee, N., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmatos, S.M., Merrick, J.M., Moreno-Palauques, R.P., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.W., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Hatteline, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL MEDLINE PUBMED COMMENT

Other ESTs: THC11414
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 176
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):100067"
/db_xref="taxon:9606"
/tissue_type="endothelial"
/clone_lib="Human Endothelial cells"

FEATURES source

Query Match 100.0%; Score 24; DB 7; Length 176;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 1 AUUCCACGAGTGCCTCAGATAGGA 24
Db 101 ATTCACGAGTGCCTCAGATAGGA 78

RESULT 5 BU963350/C

LOCUS BU963350 179 bp mRNA linear EST 21-OCT-2002
DEFINITION AGENCOURT 10616090 NIH MGC 141 Homo sapiens cDNA clone IMAGE:6744396 5', mRNA sequence.

ACCESSION BU963350

VERSION BU963350.1 GI:24192922

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 179)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

JOURNAL

Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

Plate: LCM3085 row: j column: 11

High quality sequence stop: 179.

FEATURES source

Location/Qualifiers

1. 179

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:6744396"

/tissue_type="mixed (pool of 40 RNAs)"

/lab_host="DH10B (TI-phage-resistant)"

/clone_lib="NIH_MGC_141"

/note="vector: pDNR-Lib; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggcgctctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGTATCAACGACAGTGCCTACGCGGG-3' and 5'-ATTCTAGGCGGCGGCGGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH_MGC 142). Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 24; DB 5; Length 179;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGTGCCTCAGATAGGA 24

Db 73 ATTCACGAGTGCCTCAGATAGGA 50

RESULT 6

LOCUS BG271724

DEFINITION BG271724 195 bp mRNA linear EST 20-FEB-2001
na152907.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4263757 3', mRNA sequence.

ACCESSION BG271724

VERSION BG271724.1 GI:12980154

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 195)

NCI/NIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: David B. Krizman, Ph.D.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gibco.

FEATURES

source

Location/Qualifiers

1. 195

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4263757"

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/lab_host="DH10B"
/clone_lib="NCI CGAP HN20"
/notes="Organ: normal head/neck tissue; Vector: pAMP1; mRNA
made from head/neck tissue, cDNA made by oligo-dT
priming. Directionally cloned into UDG sites.
Size-selected on agarose gel, average insert size 300 bp.
Primary library. cDNA Library Preparation: David B.
Krizman, Ph.D."

ORIGIN
Query Match 100.0%; Score 24; DB 4; Length 195;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGUGCCUACAGAUAGGA 24
Db 81 ATTCCACCAAGTGCCTCAGATAGGA 104

RESULT 7
F00105/c
LOCUS
DEFINITION
HBS21G041 STRATAGNE Human skeletal muscle cDNA library, cat.
#936215. Homo sapiens cDNA clone 21G04, mRNA sequence.
ACCESSION F00105
VERSION F00105.1 GI:707366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 196)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
7757816
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33160778698
Fax: 33160778698
Email: genexpress@genethon.fr
Single read. 18 T removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: aic-0hb08
Seq primer: (-21)M13 universal.
Location/Qualifiers
1..196
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-0hb08"
/sex="Female"
/tissue_type="skeletal muscle"
/dev_stage="19 years"
/clone_lib="STRATAGNE Human skeletal muscle cDNA library,
cat. #936215."
/notes="Organ: leg muscle; Vector: Lambda ZAP11; Tissue
from female, 19 years old, normal leg muscle. Cloning
vector is Lambda ZAP11, in vivo excision from lambda ZAP11
to pBluescript SK(+). Genexpress library reference is B. "
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Db 77 ATTCCACCAAGTGCCTCAGATAGGA 54

RESULT 8
Z38593
LOCUS
DEFINITION
HSC0HB082 normalized infant brain cDNA Homo sapiens cDNA clone
c-0hb08 3', mRNA sequence.
ACCESSION Z38593
VERSION Z38593.1 GI:560985
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 207)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
7757816
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33160778698
Fax: 33160778698
Email: genexpress@genethon.fr
Single read. 18 T removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: aic-0hb08
Seq primer: (-21)M13 universal.
Location/Qualifiers
1..207
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/clone="c-0hb08"
/sex="Female"
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/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/notes="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex:Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soaes, Psychiatry
Dept. Columbia University, USA Normalization_method:
Bento Soares, P.N.A.S in press"

ORIGIN
Query Match 100.0%; Score 24; DB 7; Length 207;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGUGCCUACAGAUAGGA 24
Db 76 ATTCCACCAAGTGCCTCAGATAGGA 99

RESULT 9
AA252742/c
LOCUS
DEFINITION
zs26a12.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:68302 5',
mRNA sequence.
ACCESSION AA252742
VERSION AA252742.1 GI:1887712
KEYWORDS EST.
SOURCE Homo sapiens (human)
```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 209)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 210
Insert Length: 738 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES
source
1..209
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_lib="NCI CGAP GCBI"
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polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATGTAAGTGGAGCGCGCCGCTCAATTTTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 100.0%; Score 24; DB 1; Length 209;
Best Local Similarity 79.2%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGUCGCUCAUAAGGA 24
|:|||||:|||||:|||||:|||||
Db 136 ATTCACCAAGTGCCTCAGTAGGA 113

RESULT 10
AA989076/c
LOCUS AA989076
DEFINITION or88e02.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602938 3',
mRNA sequence.
ACCESSION AA989076
VERSION AA989076.1 GI:3174647
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 237)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 210
Insert Length: 738 Std Error: 0.00
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/db_xref="taxon:9606"
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/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 100.0%; Score 24; DB 1; Length 237;
Best Local Similarity 79.2%; Pred. No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGUCGCUCAUAAGGA 24
|:|||||:|||||:|||||:|||||
Db 127 ATTCACCAAGTGCCTCAGTAGGA 104

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LOCUS AA148462
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mRNA sequence.
ACCESSION AA148462
VERSION AA148462.1 GI:6196358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 245)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 241.
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/tissue_type="renal cell tumor"
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/clone_lib="NCI CGAP_Kid8"

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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 100.0%; Score 24; DB 1; Length 237;
Best Local Similarity 79.2%; Pred. No. 2.3;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACGAGUCGCUCAUAAGGA 24
|:|||||:|||||:|||||:|||||
Db 127 ATTCACCAAGTGCCTCAGTAGGA 104

RESULT 11
AA148462
LOCUS AA148462
DEFINITION xfl4e04.x1 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618046 3',
mRNA sequence.
ACCESSION AA148462
VERSION AA148462.1 GI:6196358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 245)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 241.
Location/Qualifiers
1..245
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
453.500 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auuccaccaguccagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	100.0	4822	3	US-09-484-970B-106
C 3	22	91.7	211	3	US-09-506-729-51
C 4	22	91.7	1669	4	US-09-949-016-3253
C 5	22	91.7	2610	4	US-09-023-655-382
C 6	22	91.7	42075	4	US-09-949-016-14995
C 7	18.8	78.3	601	4	US-09-949-016-31983
C 8	18.8	78.3	601	4	US-09-949-016-70441
C 9	18.8	78.3	246230	4	US-09-949-016-17019
C 10	18.8	78.3	246230	4	US-09-949-016-17020
C 11	18.8	78.3	246230	4	US-09-949-016-17021
C 12	18.8	78.3	246230	4	US-09-949-016-17022
C 13	18.4	76.7	321022	4	US-09-949-016-11852
C 14	18.4	76.7	321022	4	US-09-949-016-14166
C 15	18.2	75.8	64593	4	US-09-949-016-16654
C 16	18.2	75.8	64593	4	US-09-949-016-16655
C 17	18.2	75.8	64593	4	US-09-949-016-16656
C 18	18.2	75.8	99498	4	US-09-949-016-12621
C 19	18.2	75.8	146428	4	US-09-949-016-12620
C 20	18.2	75.8	146438	4	US-09-949-016-12081
C 21	17.6	73.3	601	4	US-09-949-016-31982
C 22	17.6	73.3	601	4	US-09-949-016-31984
C 23	17.6	73.3	601	4	US-09-949-016-62026
C 24	17.6	73.3	601	4	US-09-949-016-70440
C 25	17.6	73.3	601	4	US-09-949-016-70442
C 26	17.6	73.3	1001	3	US-09-641-638-201
C 27	17.6	73.3	1001	3	US-09-641-638-202

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C 29 17.6 73.3 1001 4 US-10-170-097-202 Sequence 202, App
C 30 17.6 73.3 60002 4 US-09-949-016-12464 Sequence 12464, A
C 31 17.6 73.3 60003 4 US-09-949-016-13823 Sequence 13823, A
C 32 17.6 73.3 314798 4 US-09-949-016-13539 Sequence 13539, A
C 33 17.2 71.7 601 4 US-09-949-016-146829 Sequence 146829, A
C 34 17.2 71.7 601 4 US-09-949-016-146830 Sequence 146830, A
C 35 17.2 71.7 601 4 US-09-949-016-146831 Sequence 146831, A
C 36 17.2 71.7 601 4 US-09-949-016-15863 Sequence 15863, A
C 37 17.2 71.7 96340 4 US-09-023-905A-5 Sequence 3, Appli
C 38 16.8 70.0 3456 4 US-09-023-905A-3 Sequence 3, Appli
C 39 16.8 70.0 4382 4 US-09-949-016-14089 Sequence 14089, A
C 40 16.8 70.0 103377 4 US-09-221-298-75 Sequence 75, Appl
C 41 16.6 69.2 588 3 US-09-401-064-75 Sequence 75, Appl
C 42 16.6 69.2 675 1 US-08-707-793A-3 Sequence 3, Appli
C 43 16.6 69.2 675 1 US-08-707-792A-3 Sequence 3, Appli
C 44 16.6 69.2 675 1 US-08-707-792A-3 Sequence 1452, Ap
C 45 16.6 69.2 2129 4 US-09-016-434-1452

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ALIGNMENTS

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RESULT 1
US-09-513-999C-11204/c
; Sequence 11204, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11204
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 486
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-11204

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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUCCUACAGUAGGA 24
DB 410 ATTCCACCAGTGCCTCAGATAGGA 387

RESULT 2
US-09-484-970B-106/c
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program

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; TYPE: DNA
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match          100.0%; Score 24; DB 3; Length 4822;
Best Local Similarity 79.2%; Pred. No. 0.05;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 4099 ATCCACCAGTGCTCAGATAGGA 4076

RESULT 3
US-09-506-729-51/c
; Sequence 51, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weisman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; TITLE OF INVENTION: GRANULOCYTIC CELLS
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506.729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056.844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-51

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QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
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Db 148 ATCCACCAGTGCTCAGATAG 127

RESULT 4
US-09-949-016-3253/c
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241.755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237.768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231.498
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3253
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253

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Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
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Db 1083 ATCCACCAGTGCTCAGATAG 1062

RESULT 5
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; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
US-09-023-655-382

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Best Local Similarity 77.3%; Pred. No. 0.43;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGGCGCCUCAGAUAG 22
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0
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17020
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17020

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Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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US-09-949-016-17021/c
; Sequence 17021, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SEQ ID NO 17021
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; TYPE: DNA
; ORGANISM: Human
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; NAME/KEY: misc.feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17021

Query Match      78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 UUCCACCAGUGCCUCAGAUAGG 23
Db      134516 TTCCACCAAGTGCCTCAACAGG 134495
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; Patent No. 6812339
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 246230
; TYPE: DNA
; ORGANISM: Human
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; NAME/KEY: misc.feature
; LOCATION: (1)...(246230)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17022

Query Match      78.3%; Score 18.8; DB 4; Length 246230;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 UUCCACCAGUGCCUCAGAUAGG 23
Db      134516 TTCCACCAAGTGCCTCAACAGG 134495

RESULT 13
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; Sequence 11852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 11852
; LENGTH: 321022
; TYPE: DNA
; ORGANISM: Human
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11852

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; Sequence 14166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-14166

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RESULT 15

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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US-09-949-016-16654

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Job time : 89.5946 secs

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C 4	17	68.0	17	6	AX216295	Sequence
C 5	17	68.0	17	6	AX216587	Sequence
C 6	17	68.0	17	6	AX216842	Sequence
C 7	16.4	65.6	22	6	AX481558	Sequence
C 8	16.4	65.6	24	6	AX481559	Sequence
C 9	16	64.0	17	6	AX216586	Sequence
C 10	15.8	63.2	60	6	CQ535926	Sequence
C 11	15.4	61.6	20	6	AX225975	Sequence
C 12	15.4	61.6	51	6	AX160170	Sequence
C 13	15	60.0	17	6	AX215989	Sequence
C 14	15	60.0	60	6	CQ537946	Sequence
C 15	15	60.0	60	6	CQ550775	Sequence
C 16	14.6	58.4	24	6	CQ816744	Sequence
C 17	14.4	57.6	17	6	AR401760	Sequence
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C 19	14.4	57.6	17	6	BD057260	Enzymatic

ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1429 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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ACCESSION AX215988
VERSION AX215988.1 GI:15526031
KEYWORDS synthetic construct
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1430 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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AX216295/c 17 bp RNA linear PAT 07-SEP-2001
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DEFINITION Sequence 1737 from Patent WO0159103.
ACCESSION AX216295
VERSION AX216295.1 GI:15526356
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
Patent: WO 0159103-A 1737 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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VERSION AX216587.1 GI:15526648
KEYWORDS synthetic construct
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2029 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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ACCESSION AX216842
VERSION AX216842.1 GI:15526903
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2284 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers

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ACCESSION AX481558
VERSION AX481558.1 GI:22316472
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
AUTHORS Method for inhibiting the expression of a target gene
TITLE Patent: WO 02055693-A 172 18-JUL-2002;
JOURNAL Ribopharma AG (DE)
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VERSION AX481559.1 GI:22316473
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SOURCE synthetic construct
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1 Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
AUTHORS Method for inhibiting the expression of a target gene
TITLE Patent: WO 02055693-A 173 18-JUL-2002;
JOURNAL Ribopharma AG (DE)
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KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Blatt,L., McSwiggen,J. and Chowrira,B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 2028 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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DEFINITION Sequence 5561 from Patent WO0210449.
ACCESSION CQ535926
VERSION CQ535926.1 GI:41502190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
AUTHORS Oligonucleotide library for detecting rna transcripts and splice
TITLE variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 5561 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
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REFERENCE	Blatt,L., McSwiggen,J. and Chowrira,B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression			
AUTHORS	TITLE	nogo gene expression		
JOURNAL	Patent:	WO 0159103-A 1431 16-AUG-2001;		
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)			
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SOURCE	Homo sapiens			
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REFERENCE	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome			
AUTHORS	Title	Patent: WO 0210449-A 7581 07-FEB-2002;		
JOURNAL	Compugen Inc. (US)			
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SOURCE	Homo sapiens			
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DEFINITION	Accession	20 bp DNA		
ACCESSION	Version	GI:27264129		
KEYWORDS	Unknown.			
SOURCE	Organism	Unclassified.		
REFERENCE	Wyatt,J. and Freier,S.M. Antisense modulation of Her-1 expression			
AUTHORS	Title	Patent: US 6444465-A 38 03-SEP-2002;		
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ACCESSION	AX160170.1	GI:14541501		
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SOURCE	Homo sapiens			
ORIGIN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	Shimkets,R.A. and Leach,M. Nucleic acids containing single nucleotide polymorphisms and methods of use thereof			
AUTHORS	Title	Patent: WO 0140521-A 3498 07-JUN-2001;		
JOURNAL	Curagen Corporation (US)			
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DEFINITION	Accession	AX215989		
ACCESSION	AX215989			

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REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Paigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 20410 07-FEB-2002;
Compugen Inc. (US)
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GenCore version 5.1.6
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10	16.4	65.6	22	6 ABV78288	ABV78288 Human EGF
11	16.4	65.6	24	6 ABV78289	ABV78289 Human EGF
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C 23	14.4	57.6	17	2	AAV97320	Aav97320 Human EGF
C 24	14.4	57.6	17	8	ACC63426	Acc63426 Murine ol
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27	14.4	57.6	20	12	ADJ17838	Adj17838 Antisense
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29	14.4	57.6	20	12	ADJ17868	Adj17868 Antisense
C 30	14.4	57.6	25	10	ADC05670	Adc05670 Human Na/
C 31	14.4	57.6	25	10	ADC05669	Adc05669 Human Na/
C 32	14.4	57.6	60	6	ABN33385	Abn33385 Human spl
C 33	14.4	57.6	60	6	ABN42423	Abn42423 Human spl
34	14.2	56.8	24	6	ABL53901	AbL53901 Human rib
35	14.2	56.8	25	9	ACK21293	Ack21293 Human mic
36	14.2	56.8	28	4	AAH91639	Aah91639 Human inf
37	14.2	56.8	31	2	AAQ37571	Aaq37571 HCV conse
38	14.2	56.8	31	2	AAT64885	Aat64885 Hepatitis
C 39	14.2	56.8	37	4	AAH91211	Aah91211 Human inf
C 40	14.2	56.8	51	4	AAI79791	Aai79791 Human non
41	14.2	56.8	60	6	ABN50365	Abn50365 Human spl
42	14.2	56.8	60	6	ABN37067	Abn37067 Human spl
C 43	14	56.0	17	4	ABK00562	Abk00562 Human NOG
C 44	14	56.0	17	4	ABK02027	Abk02027 Human NOG
45	14	56.0	20	12	ADJ16733	Adj16733 Antisense

ALIGNMENTS

RESULT 1
AAC64407
ID AAC64407 standard; RNA; 25 BP.
XX AAC64407;
AC AAC64407;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:3.
XX
KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
KW stress-phosphorylated endoplasmic reticulum protein; cytosstatic;
KW gene therapy; cell growth; cellular stress response; neuron growth;
KW regulator of oxidative stress; inhibitor of neurite outgrowth;
KW axon regeneration; diagnosis; cancer; identification; antisense;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..25
FT /*tag= a
FT /note= "phosphorothioate linkages"
FT
XX WO2000060083-A1.
XX
PN 12-OCT-2000.
XX
PD
XX
PP 07-APR-2000; 2000WO-US009383.
XX
PR 08-APR-1999; 99US-0128372P.
PR 21-JUN-1999; 99US-0140331P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Wei D, Halenbeck R, Williams LT;
XX
XX WPI; 2000-665007/64.
XX
XX Novel protein associated with cell stress response useful for modulating
PT stress levels, cell growth, diagnosis and treatment of cancer and
PT malignant growth and for identifying agonists and antagonists.
XX

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic
 CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and
 CC is a modulator of the storage and exchange of calcium, cell growth and
 CC cellular stress response. It can: regulate oxidative stress; inhibit
 CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
 CC polypeptides and polynucleotides are useful for modulating stress levels
 CC and cellular stress-response, cell growth and viability, diagnosis and
 CC treatment of cancer, malignant growth and other Nogo B related diseases.
 CC Nogo B polypeptides are also useful to screen combinatorial libraries to
 CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
 CC are useful for affinity chromatography and distinguishing Nogo B
 CC polypeptides. The present sequence represents a human Nogo B
 CC phosphorothioate antisense oligonucleotide from the present invention

SQ Sequence 25 BP; 5 A; 7 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUACCUUGGAUACACCCUUG 25
 |||||
 Db 1 CUGGAUACCUUGGAUACACCCUUG 25

RESULT 2

ABK0561/c
 ID ABK00561 standard; RNA; 17 BP.
 AC ABK00561;
 DT 12-MAR-2002 (first entry)
 XX Human Nogo Hammerhead Ribozyme #561.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 XX central nervous system injury.
 XX Claim 88; Page 74; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (Nogo). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The Nogo-
 CC targeting nucleic acid is used to cleave RNA of the Nogo gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce Nogo activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC Nogo. The treatment may further comprise the use of one or more
 CC therapies. In particular, the Nogo-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of Nogo expression. The present
 CC sequence is a hammerhead ribozyme of the invention

SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 76.5%; Pred. No. 3.3e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUAGCUUGGAUACACACC 21
 |||||
 Db 17 ATAGCTTGGATCACACC 1

RESULT 3

ABK01737/c
 ID ABK01737 standard; RNA; 17 BP.
 XX ABK01737;
 XX 12-MAR-2002 (first entry)
 XX Human Nogo Zinzyme #59.
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.
 OS

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 3 G; 0 T; 5 U; 0 Other;
 Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 76.5%; Pred. No. 3.3e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 CGAUAAGCUUGAUCACA 19
 Db 17 GGATAGCTTGGATCACA 1
 RESULT 5
 ID ABRK02029 standard; RNA; 17 BP.
 XX
 AC ABRK02029;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Zinzyme #351.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 88; Page 101; 200pp; English.
 PS
 XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 68.0%; Score 17; DB 4; Length 17;
 Best Local Similarity 70.6%; Pred. No. 3.3e+02;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CUGAUAAGCUUGAUCACA 17
 Db 17 CTGGATAGCTTGGATCA 1
 RESULT 6
 ID ABRK01429/c
 XX
 AC ABRK01429;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #699.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.


```
CC sequence is a DNazyme molecule of the invention
XX Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
SQ
    Query Match      68.0%; Score 17; DB 4; Length 17;
    Best Local Similarity 76.5%; Pred. No. 3.3e+02;
    Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AGCUUGGAUCACACCCU 23
Db 17 AGCTTGGATCACACCT 1

RESULT 8
ID ADF73036/c
XX ADF73036 standard; cDNA; 58 BP.
AC ADF73036;
XX
DT 12-FEB-2004 (first entry)
XX
DE DNA sequence of the invention #6.
XX
KW human repair gene DNA polymerase beta; gene therapy; esophagus cancer;
KW ss.
OS Synthetic.
XX
XX CN1366047-A.
FN
PD 28-AUG-2002.
XX
PF 24-AUG-2001; 2001CN-00128374.
XX
PR 24-AUG-2001; 2001CN-00128374.
XX
PA (UYZH-) UNIV ZHENGZHOU.
XX
PI Dong Z, Zhao G, Zhao Q;
XX
XX WPI; 2003-240398/24.
XX
XX Human DNA polymerase beta mutant gene and its corresponding protein.
XX
PS Claim 3; Page 2; 11pp; Chinese.
XX
CC The present invention discloses a cDNA sequence of human repair gene DNA
CC polymerase beta, which is a specific representation of DNA polymerase
CC beta in esophagus cancer. The protein coded by it has fully lost the DNA
CC repair activity of DNA polymerase beta. It can be used for early
CC diagnosis and gene therapy of esophagus cancer. This sequence represents
CC a human DNA polymerase beta associated oligonucleotide
XX
SQ Sequence 58 BP; 22 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
    Query Match      66.4%; Score 16.6; DB 10; Length 58;
    Best Local Similarity 52.2%; Pred. No. 6.1e+02;
    Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
Db 38 TGGATAGCTTGGCTCACGTTCTT 16

RESULT 10
ID ABV78288/c
XX ABV78288 standard; RNA; 22 BP.
AC ABV78288;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human EGFR inhibitor dsRNA sense strand SEQ ID NO 172.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; ds.
XX
OS Homo sapiens.
XX
XX WO200255693-A2.
FN
XX 18-JUL-2002.
PD
XX
XX 09-JAN-2002; 2002WO-EP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
PR
XX 26-OCT-2001; 2001DE-01055280.
PR
XX 29-NOV-2001; 2001DE-01058411.
PR
XX 07-DEC-2001; 2001DE-01060151.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
DE
```

```
XX
KW Human; repair gene; DNA polymerase beta; oesophagus cancer;
KW DNA repair activity; gene therapy; ss.
XX
OS Unidentified.
XX
XX CN1366047-A.
FN
XX 28-AUG-2002.
PD
XX
XX 24-AUG-2001; 2001CN-00128374.
PF
XX
XX 24-AUG-2001; 2001CN-00128374.
PR
XX
XX (UYZH-) UNIV ZHENGZHOU.
PA
XX
XX Dong Z, Zhao G, Zhao Q;
PI
XX
XX WPI; 2003-240398/24.
DR
XX
XX Human DNA polymerase beta mutant gene and its corresponding protein.
PT
XX
XX Claim 3; Page 2; 11pp; Chinese.
PS
XX
CC The present invention discloses a cDNA sequence of human repair gene DNA
CC polymerase beta, which is a specific representation of DNA polymerase
CC beta in esophagus cancer. The protein coded by it has fully lost the DNA
CC repair activity of DNA polymerase beta. It can be used for early
CC diagnosis and gene therapy of esophagus cancer. This sequence represents
CC a human DNA polymerase beta associated oligonucleotide
XX
SQ Sequence 58 BP; 22 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
    Query Match      66.4%; Score 16.6; DB 10; Length 58;
    Best Local Similarity 52.2%; Pred. No. 6.1e+02;
    Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
Db 38 TGGATAGCTTGGCTCACGTTCTT 16

RESULT 10
ID ABV78288/c
XX ABV78288 standard; RNA; 22 BP.
AC ABV78288;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human EGFR inhibitor dsRNA sense strand SEQ ID NO 172.
XX
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; ds.
XX
OS Homo sapiens.
XX
XX WO200255693-A2.
FN
XX 18-JUL-2002.
PD
XX
XX 09-JAN-2002; 2002WO-EP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
PR
XX 26-OCT-2001; 2001DE-01055280.
PR
XX 29-NOV-2001; 2001DE-01058411.
PR
XX 07-DEC-2001; 2001DE-01060151.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
DE
```


XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
XX target and having an overhang.
XX
XX Claim 13; Page 40; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a dsRNA molecule related to the invention
XX
XX Sequence 22 BP; 6 A; 6 C; 5 G; 0 T; 5 U; 0 Other;
SQ

Query Match 65.6%; Score 16.4; DB 6; Length 22;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAUAGCTUGGAUCACAC 20
||| |||:|||||
Db 19 GGACAGCTTGGATCACAC 2

RESULT 11
ABV78289
ID ABV78289 standard; RNA; 24 BP.
XX
AC ABV78289;
XX
XX 15-NOV-2002 (first entry)
XX
XX Human EGFR inhibitor dsRNA antisense strand SEQ ID NO 173.
XX
XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
XX virucide; protozoacide; ds.
XX
XX Homo sapiens.
XX
XX WO200255693-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-EP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX 26-OCT-2001; 2001DE-01055280.
XX 29-NOV-2001; 2001DE-01058411.
XX 07-DEC-2001; 2001DE-01060151.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
XX Claim 13; Page 40; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1

CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a dsRNA molecule related to the invention
XX
XX Sequence 24 BP; 5 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
SQ

Query Match 65.6%; Score 16.4; DB 6; Length 24;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAUAGCTUGGAUCACAC 20
||| |||:|||||
Db 4 GGACAGCTUGGAUCACAC 21

RESULT 12
ADH72558
ID ADH72558 standard; DNA; 26 BP.
XX
XX AC ADH72558;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human probe of the invention SEQ ID NO:1454.
XX
XX human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia; ss; probe.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0386942P.
XX 07-JUN-2002; 2002US-0386971P.
XX 07-JUN-2002; 2002US-0387262P.
XX 08-JUN-2002; 2002US-0296960P.
XX 10-JUN-2002; 2002US-0387400P.
XX 10-JUN-2002; 2002US-0387535P.
XX 11-JUN-2002; 2002US-0387610P.
XX 11-JUN-2002; 2002US-0387625P.
XX 11-JUN-2002; 2002US-0387634P.
XX 11-JUN-2002; 2002US-0387668P.
XX 11-JUN-2002; 2002US-0387696P.
XX 11-JUN-2002; 2002US-0387702P.
XX 11-JUN-2002; 2002US-0387836P.
XX 11-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387933P.
XX 12-JUN-2002; 2002US-0387934P.
XX 12-JUN-2002; 2002US-0387960P.
XX 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 14-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390066P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 21-JUN-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401566P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 13-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0405182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420633P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangolli EA, Gerlach V, Gorman L, Gunther E, Guo X;
 PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malyanar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raba D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;

WPI; 2004-081935/08.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

PS Disclosure; SEQ ID NO 1454; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC is used in the exemplification of the invention.

XX SQ Sequence 26 BP; 7 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 64.8%; Score 16.2; DB 12; Length 26;

Best Local Similarity 71.4%; Pred. No. 8.4e+02;

Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CUGGAUAGCTUUGGAUCACACC 21

Dd 1 CTGGACATCTTGGAAACACACC 21

RESULT 13

ABK02028/c

ID ABK02028 standard; RNA; 17 BP.

XX AC ABK02028;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO Zinzyne #350.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

XX Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswigen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

PS Claim 88; Page 101; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention

XX SQ Sequence 17 BP; 6 A; 3 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 64.0%; Score 16; DB 4; Length 17;
 Best Local Similarity 68.8%; Pred. No. 9.9e+02; Indels 0; Gaps 0;
 Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 10 UUGAUGACACACCCUUG 25
 :|||:|||||:|
 Db 17 TTGGATCACACCTTG 2

RESULT 14
 ABN32813/c
 ID ABN32813 standard; DNA; 60 BP.

XX AC ABN32813;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:5561.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 XX splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX FN WO200210449-A2.

XX PD 07-FEB-2002.

XX PP 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

DR

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

XX Example 1; SEQ ID NO 5561; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 BP; 14 A; 13 C; 16 G; 17 T; 0 U; 0 Other;

Query Match 63.2%; Score 15.8; DB 6; Length 60;
 Best Local Similarity 68.4%; Pred. No. 1.5e+03;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGCUUGAUCACACCCUUG 25
 |::|::|::|::|::|
 Db 41 ATCTTGATCACACCCATG 23

RESULT 15
 AAD36524

ID AAD36524 standard; DNA; 20 BP.

XX AC AAD36524;

XX DT 09-AUG-2002 (first entry)

XX DE Human Her-1 antisense oligonucleotide ISIS #122133.

XX KW Human; epidermal growth factor receptor; hyperproliferative disease;
 KW Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
 XX tumour; cancer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX modified_base 1..20

FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /mod_base= OTHER
 FT /note= "2'methoxyethyl nucleotides"

FT modified_base 7

FT /mod_base= m5C
 FT modified_base 10

FT /*tag= e
FT /mod_base= m5c
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 17
FT /*tag= f
FT /mod_base= m5c
FT 19
FT /*tag= g
FT /mod_base= m5c

WO200226758-A1.

04-APR-2002.

28-SEP-2001; 2001WO-US030551.

29-SEP-2000; 2000US-00676610.

(ISIS-) ISIS PHARM INC.

Bennett CF, Wyatt JR, Freier SM;

WPI; 2002-394234/42.

Novel antisense oligonucleotide that specifically hybridizes with and inhibits nucleic acid encoding epidermal growth factor receptor, useful for treating hyperproliferative disease such as cancer or psoriasis.

Example 19; Page 45; 169pp; English.

The invention relates to an antisense oligonucleotide targetted to a nucleic acid molecule encoding human epidermal growth factor receptor (Her1) to inhibit its expression. The antisense compounds are useful for treating diseases or conditions associated with Her-1 such as hyperproliferative diseases especially cancer (lung, ovarian, colon or prostate cancer) and psoriasis. They are also useful as research reagents, diagnostics, therapeutics, kits and prophylactically e.g. to prevent or delay tumour formation. The present sequence is an antisense oligonucleotide targetted to human Her-1

Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 6; Length 20;
Best Local Similarity 76.5%; Pred.No.1.9e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAAAGCCTUGGAUCACA 19
DB 4 GGACAGCTTGGATCACA 20

Search completed: July 30, 2005, 15:45:00
Job time : 309.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:01:12 ; Search time 2428.72 Seconds
(without alignments)
391.815 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25
Sequence: 1 cuggaagcuggaaccacccug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	57.6	42	8	AQ072941 EP(2)2154
C 2	14.2	56.8	46	9	AL765810 Arabidops
C 3	14.2	56.8	60	8	AZ317154 1M0035G16
C 4	14.2	56.0	45	9	AL943467 Arabidops
C 5	13.8	55.2	55	9	CL528471 ASV13H02.
C 6	13.6	54.4	34	9	AL942366 Arabidops
C 7	13.6	54.4	51	8	BH908280 SALK_0469
C 8	13.6	54.4	58	1	AA918654 ol67f12.8
C 9	13.4	53.6	36	2	BB617639 601441590
C 10	13.4	53.6	36	8	AZ800990 2M0059H15
C 11	13.2	52.8	25	8	BH814737 SALK_0868
C 12	13.2	52.8	42	8	BH630486 1007088F1
C 13	13.2	52.8	51	8	AZ771156 1M0573C12
C 14	13.2	52.8	59	1	AA207740 mv78h05.r
C 15	13.2	52.8	59	8	AZ395181 1M0159M03
C 16	13	52.0	43	1	AA576294 ad37d06.s
C 17	13	52.0	43	1	AL763703 Arabidops
C 18	12.8	51.2	36	4	BG538454 602567160
C 19	12.8	51.2	41	9	AL762995 Arabidops
C 20	12.8	51.2	43	1	A1097835 ue40e02.y
C 21	12.8	51.2	43	1	A1491879 to01h12.x
C 22	12.8	51.2	43	8	BH901304 SALK_0743
C 23	12.8	51.2	49	1	AA168179 ms30504.r
C 24	12.8	51.2	49	9	AL765094 Arabidops

25	12.8	51.2	50	7	H60434
C 26	12.8	51.2	52	4	BJ000348
C 27	12.8	51.2	52	9	CR164369 Forward s
C 28	12.8	51.2	56	1	AL777445
C 29	12.8	51.2	57	8	CC458457
C 30	12.8	51.2	59	9	CR247136 Forward s
C 31	12.6	50.4	28	8	AZ782057 2M0021P24
C 32	12.6	50.4	31	2	AV962471
C 33	12.6	50.4	34	7	N63645
C 34	12.6	50.4	35	2	BF036425
C 35	12.6	50.4	43	9	CG869098 AC0059 Sa
C 36	12.6	50.4	43	8	BH856117 SALK_0833
C 37	12.6	50.4	56	7	H69956 yn72e10.81
C 38	12.6	50.4	57	9	CG774043 1123017A0
C 39	12.6	50.4	58	8	AZ783926 2M0026J02
C 40	12.6	50.4	60	6	CD917506 G608.105J
C 41	12.4	49.6	37	8	AZ423769 1M0203G22
C 42	12.4	49.6	50	1	AU105134 AU105134
C 43	12.4	49.6	52	4	BJ000348
C 44	12.4	49.6	52	7	CN922922 000411AEL
C 45	12.4	49.6	53	6	CB353071 ZF001-P00

ALIGNMENTS

RESULT 1
AQ072941/c
LOCUS
DEFINITION
EP(2)2154 Drosophila melanogaster EP line Drosophila melanogaster
genomic Sequence recovered from Both 5' and 3' ends of P element,
genomic sequence sequence.
ACCESSION
AQ072941
VERSION
AQ072941.1 GI:3403392
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1. (bases 1 to 42)
Liao, S.-C., Rehm, E.J. and Rubin, G.M.
Insertion site preferences of the P transposable element in
Drosophila melanogaster
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
JOURNAL
MEDLINE
20202638
PUBMED
10716700
COMMENT
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106433947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 7 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1. .42

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone lib="Drosophila melanogaster Ep line"

/note="Inverse PCR was performed on Drosophila

melanogaster strains each of which contains a single Ep

transposable element insertion. (The generation of these

insertion strains is described in Rorth P, Szabo K, Bailey

A, Lavery T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes


```

Db      12 CTGAGTAGCTGGGACACAGCGATG 36

RESULT 6
LOCUS   AL942366
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-265D06-014998, genomic survey sequence.
ACCESSION AL942366
VERSION   AL942366.1 GI:24398964
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana

REFERENCE
AUTHORS   Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE      GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL    Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE    22755829
PUBMED     12874060
AUTHORS    Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
TITLE      An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL    Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE    23117147
PUBMED     14756321
AUTHORS    Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.
TITLE      High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL    BioTechniques 35 (6), 1164-1168 (2003)
MEDLINE    14682050
PUBMED     14682050
AUTHORS    Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.
TITLE      Direct Submission
JOURNAL    Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT    This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atlg48900. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES             Location/Qualifiers
     1..34
         /organism="Arabidopsis thaliana"
         /mol_type="genomic DNA"
         /strain="Columbia 0"
         /db_xref="taxon:3702"
         /clone="GK-265D06-014998"
         /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
         /ecotype="Col-0"
         /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match      54.4%; Score 13.6; DB 9; Length 34;
Best Local Similarity 55.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
LOCUS   BH908280
DEFINITION Arabidopsis thaliana T-DNA insertion lines
ACCESSION BH908280
VERSION   BH908280.1 GI:22721213
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana

REFERENCE
AUTHORS   Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL    Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@alk.edu
            This is single pass sequence recovered from the left border of T-DNA.

FEATURES             Location/Qualifiers
     1..51
         /organism="Arabidopsis thaliana"
         /mol_type="genomic DNA"
         /ecotype="Col-0"
         /db_xref="taxon:3702"
         /clone="SALK_046972.17.10.x"
         /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
         /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      54.4%; Score 13.6; DB 8; Length 51;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db      5 AUAGCUUGGACACACCCUU 24
        31 ATAGATTGGGTCAATCAIT 50

RESULT 8
LOCUS   AA918654
DEFINITION Arabidopsis thaliana T-DNA insertion lines
ACCESSION AA918654
VERSION   AA918654.1 GI:3058544
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

Query Match      54.4%; Score 13.6; DB 9; Length 34;
Best Local Similarity 55.0%; Pred. No. 1.2e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 58)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 519 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
FEATURES Location/Qualifiers
 source 1..58
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1534703"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_Kid3"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 54.4%; Score 13.6; DB 1; Length 58;
 Best Local Similarity 70.0%; Pred. No. 1.3e+05;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGAUAGCGTGGATCACTCC 23
 |||||:|||||
 Db 4 GGAUAGCGTGGATCACTCC 23

RESULT 9
 BE617639 36 bp mRNA linear EST 20-OCT-2000
LOCUS 60144159071 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845711 3', mRNA sequence.
DEFINITION BE617639
ACCESSION BE617639.1 GI:9888577
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Htp: L1AM9557 row: c column: 24
 High quality sequence start: 18
 High quality sequence stop: 36.

FEATURES

Location/Qualifiers
 source 1..36
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3845711"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_65"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 53.6%; Score 13.4; DB 2; Length 36;
 Best Local Similarity 56.5%; Pred. No. 1.5e+05;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCU 23

Db 7 CGGACGAGTTTGGGTCCACCCCT 29

RESULT 10

AZ800990 36 bp DNA linear GSS 16-FEB-2001
 2M0059H15F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0059H15 F, genomic survey sequence.

ACCESSION AZ800990

VERSION AZ800990.1 GI:12953313

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 36)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: H column: 15

Seq primer: CGGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

FEATURES

source

1..36
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0059H15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="vector: PMD42nv; Purified genomic DNA from M.

AA207740/c	59 bp	mrna	linear	EST 12-MAR-1997
LOCUS	mv78h05.r1	GuayWoodford	Beier	Mus musculus kidney stage 7 Mus musculus cDNA
DEFINITION	clone IMAGE:661209 5'	similar to gb:X13661	Mouse	mrna for elongation factor 1-alpha (MOUSE);, mRNA sequence.
ACCESSION	AA207740			
VERSION	AA207740.1	GI:1804254		
KEYWORDS	EST.			
SOURCE	Mus musculus	(house mouse)		
ORGANISM	Mus musculus			
REFERENCE	1	(bases 1 to 59)		
AUTHORS	Marrs,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.			
TITLE	The WashU-HMMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:407057 Trace considered overall poor quality Seq primer: -28m13 rev1 ET from Amersham			

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FEATURES
source
1. 59
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:661209"
/tissue_type="kidney"
/dev_stage="juvenile (7 days old)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="GuayWoodford Beller mouse kidney day 7"
/notes="Organ: kidney; Vector: pBluescript SK-; Site: 1;
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
~5' adaptor sequence: 5' GAATTCGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Library provided
by Lisa Guay-Woodford."

ORIGIN

Query Match          52.8%;   Score 13.2;   DB 1;   Length 59;
Best Local Similarity 66.7%;   Pred. No. 1.9e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      5  AUAAGCUUGGAUACACCC 22
      |  ||||: ||: |||||
Db      46  ACAGCTTTGATGACCC 29

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RESULT 15	AZ395181	59 bp	DNA	linear	GSS 03-OCT-2000
LOCUS	AZ395181				
DEFINITION	1M0159M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0159M03 F, genomic survey sequence.				
ACCESSION	AZ395181				
VERSION	AZ395181				
KEYWORDS	AZ395181.1	GI:10510253			
SOURCE	GSS.				
ORGANISM	Mus musculus	(house mouse)			
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

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REFERENCE
AUTHORS
1 (bases 1 to 59)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0159 row: M column: 03
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 59.
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1..59
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0159M03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 59;
Best Local Similarity 61.1%; Pred. No. 1.9e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 UGAUNAGCTUUGAUCACA 19
:|:|:|:|:|:|:|:|:|:|
Db 7 TGAATAGCTGGATTACA 24

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ORIGIN

Query Match	52.8%	Score 13.2;	DB 8;	Length 59;
Best Local Similarity	61.1%;	Pred. No. 1.9e+05;		
Matches 11;	Conservative	4;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 2 UGGAUAGCUUGAUCACA 19
 : | | | | : | | |
Db 7 TGAATAGCTGGGATTACA 24

Search completed: July 30, 2005, 18:20:42
Job time : 2432.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:05:52 ; Search time 87.8378 Seconds
(without alignments)
465.710 Million cell updates/sec

Title: US-09-544-776-3

Perfect score: 25

Sequence: 1 cuggaagcuggaucacacccuug 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	61.6	20	3	US-09-676-610B-38
C 2	14.4	57.6	17	3	US-08-985-162-100
C 3	14.4	57.6	17	3	US-09-401-063-100
4	14.2	56.8	31	1	US-08-240-547-3
C 5	14	56.0	40	3	US-09-485-737B-12
C 6	14	56.0	40	4	US-10-071-485-12
C 7	14	56.0	57	2	US-08-750-703-10
C 8	13.6	54.4	25	4	US-09-396-196G-75584
9	13.6	54.4	25	4	US-09-396-196G-94761
10	13.6	54.4	56	3	US-08-513-968-39
C 11	13.4	53.6	18	2	US-09-205-860-53
C 12	13.4	53.6	25	4	US-09-396-196G-23284
13	13.4	53.6	25	4	US-09-396-196G-124476
14	13.4	53.6	40	5	PCT-US91-00909-10
C 15	13.4	53.6	43	5	PCT-US91-00909-13
16	13.4	53.6	56	4	US-09-513-999C-18929
C 17	13.4	53.6	60	3	US-08-729-601A-41
C 18	13.2	52.8	47	4	US-09-422-978-1184
C 19	13.2	52.8	50	1	US-08-207-901-66
C 20	13.2	52.8	60	1	US-08-484-182-177
C 21	13	52.0	25	4	US-09-396-196G-113155
22	13	52.0	26	3	US-08-640-737-13
23	13	52.0	27	3	US-09-020-846-32
C 24	13	52.0	33	1	US-08-417-476-21
C 25	13	52.0	34	3	US-09-162-021B-18
C 26	13	52.0	39	1	US-08-324-243-25
C 27	13	52.0	39	1	US-08-532-390-25

C 28 13 52.0 39 3 US-08-717-294-25 Sequence 25, Appl
C 29 13 52.0 39 5 PCT-US95-11511-25 Sequence 25, Appl
C 30 13 52.0 60 5 PCT-US95-11985A-9 Sequence 9, Appl
C 31 12.8 51.2 19 4 US-08-983-605-168 Sequence 168, App
C 32 12.8 51.2 20 4 US-09-422-978-10858 Sequence 10858, A
C 33 12.8 51.2 23 3 US-08-276-968A-28 Sequence 28, Appl
C 34 12.8 51.2 25 4 US-09-274-752D-16 Sequence 16, Appl
C 35 12.8 51.2 25 4 US-09-396-196G-76462 Sequence 76462, A
C 36 12.8 51.2 26 4 US-09-439-813-4 Sequence 4, Appl
C 37 12.8 51.2 26 4 US-09-439-813-6 Sequence 6, Appl
C 38 12.8 51.2 28 3 US-09-012-097A-21 Sequence 21, Appl
C 39 12.8 51.2 29 4 US-09-791-105B-28 Sequence 28, Appl
C 40 12.8 51.2 33 3 US-09-461-697-134 Sequence 134, App
C 41 12.8 51.2 36 4 US-09-978-758-17 Sequence 17, Appl
C 42 12.8 51.2 40 3 US-08-961-083-297 Sequence 297, App
C 43 12.8 51.2 40 4 US-09-536-784-297 Sequence 297, App
C 44 12.8 51.2 48 4 US-09-591-466C-10 Sequence 10, Appl
C 45 12.8 51.2 50 1 US-08-207-901-65 Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-676-610B-38
; Sequence 38, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: R7S-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-676-610B-38

Query Match 61.6%; Score 15.4; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.4e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GGAGCUGGAGUACACA 19
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Db 4 GGACAGCTTGGATCACA 20

RESULT 2

US-08-985-162-100/c
; Sequence 100, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```

; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-401-063-100

Query Match 57.6%; Score 14.4; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 1; Indels

Qy 5 AUAGCUUGAUCACAC 20
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Db 17 ACAGCTTGGATCACAC 2

RESULT 4
US-08-240-547-3
; Sequence 3, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D. Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-240-547-3

Query Match 55.8%; Score 14.2; DB 1; Length 31;

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Best Local Similarity 63.2%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 7 AGCUUGAUCACACCCUUG 25
|||::|||::|||::|||
Db 4 AGCTTAGATCACTCCCTG 22

RESULT 5
US-09-485-737B-12/c
; Sequence 12, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: GENOMIC
US-09-485-737B-12

Query Match 56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGAUCACACCCU 23
|||::|||::|||::|||
Db 34 TGGATGGTTGGATCAACACCT 13

RESULT 6
US-10-071-485-12/c
; Sequence 12, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 40
; TYPE: DNA
; ORGANISM: UNKNOWN
; FEATURE:

; OTHER INFORMATION: GENOMIC
US-10-071-485-12

Query Match 56.0%; Score 14; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGAUCACACCCU 23
|||::|||::|||::|||
Db 34 TGGATGGTTGGATCAACACCT 13

RESULT 7
US-08-750-703-10/c
; Sequence 10, Application US/08750703
; Patent No. 5891633
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R.
; TITLE OF INVENTION: DEFECTS IN DRUG
; TITLE OF INVENTION: METABOLISM
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Ave.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,703
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07605
; FILING DATE: 16-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dorothy R. Auth
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4196PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; NAME/KEY: F4 primer
; LOCATION:
; OTHER INFORMATION: Primer used for CYP2A6
; OTHER INFORMATION: genotyping.
US-08-750-703-10

Query Match 56.0%; Score 14; DB 2; Length 57;
Best Local Similarity 59.1%; Pred. No. 2.4e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CUGAUGAGCUUGAUCACACCC 22
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Db 41 CTGCCTAGCTTGGACACAGCC 20

RESULT 8
US-09-396-196G-75584/c
; Sequence 75584, Application US/09396196G

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75584

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 55.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      6 UAGCUUGGAUCACACCCUUG 25
Db      :|||:|||:|||:|||
        23 TAGCTGGGATAACATACATG 4

RESULT 9
US-09-396-196G-94761
; Sequence 94761, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-94761

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 55.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      6 UAGCUUGGAUCACACCCUUG 25
Db      :|||:|||:|||:|||
        2 TATCTGGGACCAAACTTG 21

RESULT 10
US-08-513-968-39
; Sequence 39, Application US/08513968
; Patent No. 611413
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
```

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; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..56
US-08-513-968-39

Query Match      54.4%; Score 13.6; DB 3; Length 56;
Best Local Similarity 55.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 CUGGAUGCUUGGAUCACAC 20
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RESULT 11
US-09-205-860-53/c
; Sequence 53, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-53

Query Match      53.6%; Score 13.4; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 4e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CUGGAUAGCUUGGAU 15
:||||| |::|||:
Db 16 CTGGATACCTGGAT 2

RESULT 12
US-09-396-196G-23284
; Sequence 23284, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23284
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-23284

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 47.8%; Pred. No. 4.2e+03;
Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
:||||| |::|||:
Db 2 TGCATTGCTAGTGTCACAGCCTT 24

RESULT 13
US-09-396-196G-124476
; Sequence 124476, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124476
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124476

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.3%; Pred. No. 4.2e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 11 UGGAUCACACCCUUG 25
:||||| |::|||:
Db 4 TGGATCACACCCGTG 18

RESULT 14
PCT-US91-00909-10
; Sequence 10, Application PC/TUS9100909
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; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-10

Query Match 53.6%; Score 13.4; DB 5; Length 40;
Best Local Similarity 52.2%; Pred. No. 4.5e+03;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
:||||| |::|||:
Db 11 TGAGTAGCAACGATCATACCTT 33

RESULT 15
PCT-US91-00909-13/c
; Sequence 13, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-13

Query Match      53.6%; Score 13.4; DB 5; Length 43;
Best Local Similarity 52.2%; Pred.No. 4.5e+03;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      2 UGGAUAGCUUGGAUCACACCCUU 24
Db      28 TGAGTAGCAACGATCATACCTT 6
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Search completed: July 30, 2005, 18:25:12
Job time : 89.8378 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:54:37 ; Search time 718.243 Seconds
(without alignments)
1686.588 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacuacaggaucacgaugccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	16.2	64.8	42	6	A32288 DNA probe (
C 3	16.2	64.8	59	6	A32049 DNA probe (
C 4	16.2	64.8	59	6	A32067 DNA probe (
C 5	16.2	64.8	60	6	CQ544937 Sequence
C 6	16.2	64.8	17	6	AX215126 Sequence
C 7	15.6	62.4	33	6	AR365650 Sequence
C 8	15.6	62.4	33	6	AR365669 Sequence
C 9	15.6	62.4	34	6	AR365637 Sequence
C 10	15.6	62.4	39	6	AR365666 Sequence
C 11	15.4	61.6	20	6	BD134588
C 12	15.0	60.0	17	6	AX215125
C 13	15.0	60.0	17	6	AX216000
C 14	15.0	60.0	60	6	CQ536812 Sequence
C 15	14.8	59.2	23	6	AX539243 Sequence
C 16	14.8	59.2	38	6	AR254609 Sequence
C 17	14.6	58.4	42	6	ES9732 Method for
C 18	14.4	57.6	21	6	BD012596 Human cyt
C 19	14.4	57.6	51	11	BX088624 Arabidops

20	14.2	56.8	60	6	CQ537523	CQ537523 Sequence
C 21	14	56.0	17	6	AX217202	AX217202 Sequence
C 22	14	56.0	20	6	AX247495	AX247495 Sequence
C 23	14	56.0	24	6	BD073932	BD073932 RTD recep
C 24	14	56.0	26	6	AX099785	AX099785 Sequence
C 25	14	56.0	32	6	AX786475	AX786475 Sequence
C 26	14	56.0	34	6	AR365647	AR365647 Sequence
C 27	14	56.0	39	6	AR365667	AR365667 Sequence
C 28	14	56.0	48	6	BD222069	BD222069 SH2 domai
C 29	14	56.0	48	6	AR179726	AR179726 Sequence
C 30	14	56.0	54	6	AX927857	AX927857 Sequence
C 31	14	56.0	54	8	AJ719032	AJ719032 Nicotiana
C 32	14	56.0	60	6	BD175864	BD175864 A method
C 33	14	56.0	60	6	CQ547543	CQ547543 Sequence
C 34	14	56.0	60	6	AX404737	AX404737 Sequence
C 35	13.8	55.2	22	6	ES9733	ES9733 Method for
C 36	13.8	55.2	27	6	AR564905	AR564905 Sequence
C 37	13.8	55.2	36	6	AR011196	AR011196 Sequence
C 38	13.8	55.2	36	6	ES4595	ES4595 Herpesvirus
C 39	13.8	55.2	36	6	117834	117834 Sequence 64
C 40	13.8	55.2	59	6	AR236928	AR236928 Sequence
C 41	13.8	55.2	60	6	CQ539376	CQ539376 Sequence
C 42	13.8	55.2	60	6	CQ543926	CQ543926 Sequence
C 43	13.8	55.2	60	6	CQ548098	CQ548098 Sequence
C 44	13.6	54.4	25	6	AR435430	AR435430 Sequence
C 45	13.6	54.4	25	6	AR435431	AR435431 Sequence

ALIGNMENTS

RESULT 1
A32068/c
LOCUS A32068 42 bp DNA linear PAT 08-DEC-1995
DEFINITION DNA probe (A.salmonicida) from patent EP0395292.
ACCESSION A32068
VERSION A32068.1 GI:1249523
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Barry,T.G., Gannon,B.X. and Powell,R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 43 31-OCT-1990;
Barry, Thomas Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard; Powell, Richard; Bernard Francis Xavier; BIORESEARCH IRELAND; Gannon, Bernard Francis Xavier; BOLAS (trading as BioResearch Ireland) - The Irish Science and Technology Agency; Powell, Richard; UNIVERSITY COLLEGE GALWAY

FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 42;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUCCAGAUAGCC 24

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Db 28 CTACAGGATTCACAGATGC 8

RESULT 2

A32288/c
LOCUS A32288 42 bp DNA linear PAT 08-DEC-1995
DEFINITION DNA probe (A.salmonica) from patent EP0395292.
ACCESSION A32288

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VERSION A32288.1 GI:1249529
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 42)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 49 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
FEATURES
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/organism="synthetic construct"
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ORIGIN
Query Match 64.8%; Score 16.2; DB 6; Length 42;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 CUUCAGGAUCCAGAUAGCC 24
Db 28 CTCAGGATTCAGACATGTC 8
RESULT 3
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LOCUS DNA probe (A.hydrophila) from patent EP0395292.
DEFINITION A32049
ACCESSION A32049
VERSION A32049.1 GI:1249504
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 59)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 24 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
FEATURES
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Best Local Similarity 66.7%; Pred. No. 4.7e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 CUUCAGGAUCCAGAUAGCC 24
Db 28 CTCAGGATTCAGACATGTC 8
RESULT 4
A32067/c
LOCUS DNA probe (A.hydrophila) from patent EP0395292.
DEFINITION A32067
ACCESSION A32067
VERSION A32067.1 GI:1249522
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 59)
AUTHORS Barry, T.G., Gannon, B.X. and Powell, R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 42 31-OCT-1990;
IRELAND; Powell, Richard; Gannon, Bernard Francis Xavier; BIORESEARCH
Gerard; Gannon, Bernard Francis Xavier; BIORESEARCH IRELAND;
Powell, Richard; UNIVERSITY COLLEGE GALWAY; Barry, Thomas Gerard;
Gannon, Bernard Francis Xavier; EOLAS (trading as BioResearch
Ireland) - The Irish Science and Technology Agency; Powell,
Richard; UNIVERSITY COLLEGE GALWAY
FEATURES
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/mol_type="unassigned DNA"
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Best Local Similarity 57.1%; Pred. No. 4.7e+03;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 5 UUCAGGAUCCAGAUAGCC 25
Db 23 TTCAGGATTCAGATATCC 3
RESULT 6
AX215126/c
LOCUS RNA
DEFINITION AX215126
ACCESSION AX215126
VERSION AX215126.1 GI:15525169
KEYWORDS

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ORIGIN	/mol_type="genomic DNA"									
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Best Local Similarity	54.5%;	Pred. No. 9.3e+03;								
Matches 12;	Conservative 6;	Mismatches 4;	Indels 0;	Gaps 0;						
QY	4	CUCVAGGAUCCAGAUAGCCC 25								
		::: : : :								
Db	9	CTTCTGGATTACCGGTATGCC 30								
		::: : : :								
RESULT 9										
AR365637/c										
LOCUS	AR365637	34 bp	DNA	linear	PAT 03-SEP-2003					
DEFINITION	Sequence 4 from patent US 5519127.									
ACCESSION	AR365637									
VERSION	AR365637.1	GI:34429549								
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 34)									
AUTHORS	Shah,J., Buharin,A. and Lane,D.J.									
TITLE	Nucleic acid probes for the detection of Pneumocystis carinii									
JOURNAL	Patent: US 5519127-A 4 21-MAY-1996;									
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Best Local Similarity	54.5%;	Pred. No. 9.3e+03;								
Matches 12;	Conservative 6;	Mismatches 4;	Indels 0;	Gaps 0;						
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Db	26	CTTCTGGATTACCGGTATGCC 5								
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RESULT 10										
AR365666										
LOCUS	AR365666	39 bp	DNA	linear	PAT 03-SEP-2003					
DEFINITION	Sequence 33 from patent US 5519127.									
ACCESSION	AR365666									
VERSION	AR365666.1	GI:34429578								
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 39)									
AUTHORS	Shah,J., Buharin,A. and Lane,D.J.									
TITLE	Nucleic acid probes for the detection of Pneumocystis carinii									
JOURNAL	Patent: US 5519127-A 33 21-MAY-1996;									
FEATURES	Location/Qualifiers									
source	1..39									
	/organism="unknown"									
	/mol_type="genomic DNA"									
ORIGIN										
Query Match	62.4%;	Score 15.6;	DB 6;	Length 39;						
Best Local Similarity	54.5%;	Pred. No. 9.3e+03;								
Matches 12;	Conservative 6;	Mismatches 4;	Indels 0;	Gaps 0;						
QY	4	CUCVAGGAUCCAGAUAGCCC 25								
		::: : : :								
Db	10	CTTCTGGATTACCGGTATGCC 31								
		::: : : :								
RESULT 11										
BD134588/c										
LOCUS	BD134588	20 bp	DNA	linear	PAT 18-SEP-2002					

```

DEFINITION Dioxin receptor gene and utilization thereof.
ACCESSION BD134588
VERSION BD134588.1 GI:23229533
KEYWORDS JP 2002045188-A/5
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Oe,N.
TITLE Dioxin receptor gene and utilization thereof
JOURNAL Patent: JP 2002045188-A 5 12-FEB-2002;
COMMENT SUMITOMO CHEMICAL CO LTD
OS Artificial Sequence
PN JP 2002045188-A/5
PD 12-FEB-2002
PP 04-AUG-2000 JP 2000236762
PI NORIHISA OE
PC C12N15/09,C07K14/705,C12N5/10,C12P21/02,C12Q1/02,PC
GOIN33/566,
PC G01N33/68//(C12N5/10,C12R1:93),(C12P21/02,C12R1:93),C12N15/00,
C12N5/00,
PC (C12N5/00,C12R1:93)
CC Designed oligonucleotide primer for PCR
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 61.6%; Score 15.4; DB 6; Length 20;
Best Local Similarity 70.8%; Pred. No. 1.1e+04;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAACUCCAGGUAUCCAG 17
17 CAACTTCAGGATCCCG 1
Db
RESULT 12
AX215125/c
LOCUS AX215125 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 567 from Patent WO0159103.
ACCESSION AX215125
VERSION AX215125.1 GI:15525168
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 567 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
ORIGIN
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Best Local Similarity 73.3%; Pred. No. 1.8e+04;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACUUCAGGAUCCAGAUGCC 25
8 ACATCAGGTTCCAGACTAGCC 30
Db
RESULT 15
AUUCCAGGAUCCAGAUGCC 25
LOCUS AX539243
QY 11 AUUCCAGGAUCCAGAUGCC 25
11 AUUCCAGGAUCCAGAUGCC 25
Db
RESULT 13
AX216000/c
LOCUS AX216000 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1442 from Patent WO0159103.
ACCESSION AX216000
VERSION AX216000.1 GI:15526043
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1442 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
ORIGIN
Query Match 60.0%; Score 15; DB 6; Length 17;
Best Local Similarity 73.3%; Pred. No. 1.8e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 10 GAUUCAGGAUCCAG 24
15 GATTCAGATATGCC 1
Db
RESULT 14
CQ536812
LOCUS CQ536812 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6447 from Patent WO0210449.
ACCESSION CQ536812
VERSION CQ536812.1 GI:41503076
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shohhan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 6447 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 60.0%; Score 15; DB 6; Length 60;
Best Local Similarity 65.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACUUCAGGAUCCAGAUGCC 25
8 ACATCAGGTTCCAGACTAGCC 30
Db
RESULT 15
AX539243
LOCUS AX539243 23 bp DNA linear PAT 23-NOV-2002
QY 11 AUUCCAGGAUCCAGAUGCC 25
11 AUUCCAGGAUCCAGAUGCC 25

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Search completed: July 30, 2005, 16:20:40
Job time : 720.243 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:18:17 ; Search time 307.77 Seconds
(without alignments)
480.857 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	25	100.0	25	3	AAC64408	Human Nog
2	16.2	64.8	60	6	ABN41824	Human spi
3	16	64.0	17	4	ABK00568	Human NOG
4	16	64.0	41	12	ADL64316	Human sin
5	15.8	63.2	19	13	ADR79899	Human apo
6	15.8	63.2	19	13	ADR77241	Human apo
7	15.8	63.2	19	13	ADR80185	Human apo
8	15.8	63.2	19	13	ADR76955	Human apo
9	15.8	63.2	20	10	AAQ48330	Apo B3500
10	15.6	62.4	34	2	AAQ10823	Pneumocys
11	15.6	62.4	34	2	AAT42447	Probe 148
12	15.6	62.4	41	6	ABL40079	Phosphoen
13	15.4	61.6	20	6	ABL54676	Cricetulu
14	15	60.0	17	4	ABK00567	Human NOG
15	15	60.0	17	4	ABK01442	Human NOG
16	15	60.0	60	6	ABN33699	Human spi
17	14.8	59.2	23	6	ABs66695	Human mul
18	14.8	59.2	38	2	AAT14558	Cytotacti
19	14.6	58.4	24	12	ADN75060	C japonic
20	14.6	58.4	34	10	ADF41788	Bacillus

C	21	14.6	58.4	42	3	AAA62887	Forward P
C	22	14.6	58.4	45	2	AAQ66143	DNA-polym
C	23	14.6	58.4	47	12	ADN11426	Adn11426 FLJ14528
	24	14.4	57.6	21	5	AAF92390	T7 clone
	25	14.4	57.6	32	1	AAK92390	Sequence
C	26	14.4	57.6	33	12	ADJ63889	Plant lip
C	27	14.4	57.6	41	12	ADL64169	Human sin
C	28	14.2	56.8	29	3	AAZ88270	Sec B nuc
	29	14.2	56.8	50	6	ABZ00890	Human leu
	30	14.2	56.8	51	13	ADR35716	Human nic
	31	14.2	56.8	51	13	ADR35715	Human nic
	32	14.2	56.8	51	13	ADR35713	Human nic
	33	14.2	56.8	51	13	ADR35714	Human nic
	34	14.2	56.8	60	6	ABN34410	Human spl
C	35	14	56.0	17	4	ABK02644	Human NOG
C	36	14	56.0	20	4	ABL58226	Virulence
	37	14	56.0	24	2	AAZ25095	PCR prime
	38	14	56.0	26	4	AAQ03304	Reverse p
	39	14	56.0	27	2	AAZ28212	Tumour an
	40	14	56.0	27	10	ADC82787	DNA seque
	41	14	56.0	32	8	ACC43414	PCR prime
C	42	14	56.0	34	2	AAQ10833	Pneumocys
C	43	14	56.0	34	2	AAT42445	Probe 149
C	44	14	56.0	41	6	ABL40078	Phosphoen
	45	14	56.0	47	6	ABK52807	Human pro

ALIGNMENTS

RESULT 1

AAC64408
ID AAC64408 standard; RNA; 25 BP.

XX AAC64408;

XX 08-FEB-2001 (first entry)

XX Human Nogo B phosphorothioate antisense oligonucleotide SEQ ID NO:4.

XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;
XX stress-phosphorylated endoplasmic reticulum protein; cytoskeletal;
XX gene therapy; cell growth; cellular stress response; neuron growth;
XX regulator of oxidative stress; inhibitor of neurite outgrowth;
XX axon regeneration; diagnosis; cancer; identification; antisense;
XX phosphorothioate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..25

FT /tag= a
FT /note= "phosphorothioate linkages"

XX WO2000060083-A1.

XX 12-OCT-2000.

XX 07-APR-2000; 2000WO-US009383.

XX 08-APR-1999; 99US-0128372P.

XX 21-JUN-1999; 99US-0140331P.

XX (CHIR) CHIRON CORP.

XX Wei D, Halenbeck R, Williams LT;

XX WPI; 2000-665007/64.

XX Novel protein associated with cell stress response useful for modulating
XX stress levels, cell growth, diagnosis and treatment of cancer and
XX malignant growth and for identifying agonists and antagonists.

```

PS Claim 25; Page 32; 68pp; English.
XX
CC The present invention describes a human stress-phosphorylated endoplasmic
CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and
CC is a modulator of the storage and exchange of calcium, cell growth and
CC cellular stress response. It can: regulate oxidative stress; inhibit
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B
CC polypeptides and polynucleotides are useful for modulating stress levels
CC and cellular stress-response, cell growth and viability, diagnosis and
CC treatment of cancer, malignant growth and other Nogo B related diseases.
CC Nogo B polypeptides are also useful to screen combinatorial libraries to
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides
CC are useful for affinity chromatography and distinguishing Nogo B
CC polypeptides. The present sequence represents a human Nogo B
CC phosphothioate antisense oligonucleotide from the present invention
XX
SQ Sequence 25 BP; 7 A; 8 C; 4 G; 0 T; 6 U; 0 Other;
Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGGCC 25
   |||||
Db 1 CAACUUCAGGAUCCAGAUAGGCC 25

RESULT 2
ABN41824/c
ID ABN41824 standard; DNA; 60 BP.
XX
AC ABN41824;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14572.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUTEN INC.
XX
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX
DR WPI; 2002-257383/30.
XX
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX
PS Example 1; SEQ ID NO 14572; 47pp; English.
XX
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or

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CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 12 A; 13 C; 13 G; 22 T; 0 U; 0 Other;
Query Match 64.8%; Score 16.2; DB 6; Length 60;
Best Local Similarity 57.1%; Pred. No. 9e+02;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAUAGGCC 25
   :||| |::|||::|: |||
Db 23 TTCACGGTTCAGATATCCC 3

RESULT 3
ABK00568/c
ID ABK00568 standard; RNA; 17 BP.
XX
AC ABK00568;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human Nogo Hammerhead Ribozyme #568.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberyne; zinyne; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
PN WO200159103-A2.
XX
XX
PD 16-AUG-2001.
XX
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
XX
PR 11-FEB-2000; 2000US-0181797P.
XX
PR 28-FEB-2000; 2000US-0185516P.
XX
PR 06-MAR-2000; 2000US-0187128P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAY/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite

```

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

XX Claim 88; Page 75; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention

XX Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 64.0%; Score 16; DB 4; Length 17;
 Best Local Similarity 75.0%; Pred. No. 9.4e+02;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAUUCAGCAUAUUGCCC 25

Db 16 GATTCAGATATGCC 1

RESULT 4

ADL64316/c

XX ADL64316 standard; DNA; 41 BP.

XX AC ADL64316;

XX DT 20-MAY-2004 (first entry)

XX DE Human single nucleotide polymorphism (SNP) #239.

XX ss; human; single nucleotide polymorphism; SNP;
 KW Cl S subcomponent protein; ClS; alanyl aminopeptidase protein; ANPEP;
 KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
 KW angioedema; angioedema-like disorder; paternity testing;
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
 KW coronary artery disease; arteriosclerosis; hypersensitivity;
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
 KW cancer; ANPEP.

XX Homo sapiens.

OS

XX

PN US2004033582-A1.

XX 19-FEB-2004.

XX 03-JUN-2003; 2003US-00453827.

XX 03-JUN-2002; 2002US-0384980P.

XX (EDMO//) EDMONDS M.

XX (HUIL//) HUI L.

XX (PERR//) PERRONE M.

XX (POWE//) POWELL J R.

XX (RAMA//) RAMANATHAN C S.

XX (SWAN//) SWANSON B.

XX (TSUC//) TSUCHIHASHI Z.

XX (ZERB//) ZERBA K.

XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;

XX Tsuchihashi Z, Zerba K;

XX WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a

PT specific location, useful in paternity testing, genetic analysis or

PT diagnosing, preventing or treating cardiovascular diseases e.g.

PT angioedema or angina pectoris.

XX Claim 3; SEQ ID NO 239; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a
 CC human gene encoding a protein, such as the Cl, S subcomponent protein
 CC (ClS), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
 CC protein (MEPIB), the aminopeptidase P-like protein (XPN-PEPL), the tissue
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
 CC including the alleles, reference alleles and alternate alleles of the
 CC single nucleotide polymorphisms, listed in the specification. The
 CC polymorphic position resides in a (non) coding position within the genomic
 CC sequence of the gene. The polymorphic position residing in a coding
 CC position results in a missense or silent mutation of the translated
 CC product of the gene. The polymorphic position residing in a non-coding
 CC position resides within the untranslated region or an intronic region of
 CC the gene. Constructing haplotypes using the nucleic acids above further
 CC comprises using the haplotypes to identify an individual for the presence
 CC of a disease phenotype, and correlating the presence of the disease
 CC phenotype with the haplotype. The disease phenotype is angioedema or an
 CC angioedema-like disorder. The nucleic acids, primers and probes are
 CC useful in phenotype correlations, paternity testing, medicine and genetic
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
 CC stroke, embolism, thrombosis, coronary artery disease or
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
 CC present sequence represents a human single nucleotide polymorphism (SNP)
 CC of the invention.

XX Sequence 41 BP; 9 A; 5 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 64.0%; Score 16; DB 12; Length 41;

Best Local Similarity 58.3%; Pred. No. 1.1e+03;

Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGCAUAUUGCCC 25

Db 34 AACTACAGGATTACACATCTGTC 11

RESULT 5

ADR79899/c

ID ADR79899 standard; DNA; 19 BP.

XX ADR79899;
 XX 16-DEC-2004 (first entry)
 XX Human apolipoprotein B (ApoB) oligonucleotide seqid 4395.
 XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
 XX OS Homo sapiens.
 XX WO2004080406-A2.
 XX 23-SEP-2004.
 XX 08-MAR-2004; 2004WO-US007070.
 XX 07-MAR-2003; 2003US-0452682P.
 XX 12-MAR-2003; 2003US-0454265P.
 XX 13-MAR-2003; 2003US-0454962P.
 XX 13-MAR-2003; 2003US-0455050P.
 XX 14-APR-2003; 2003US-0462894P.
 XX 17-APR-2003; 2003US-0463772P.
 XX 25-APR-2003; 2003US-0465665P.
 XX 25-APR-2003; 2003US-0465802P.
 XX 09-MAY-2003; 2003US-0469612P.
 XX 08-AUG-2003; 2003US-0493986P.
 XX 11-AUG-2003; 2003US-0494597P.
 XX 26-SEP-2003; 2003US-0506341P.
 XX 09-OCT-2003; 2003US-0510246P.
 XX 10-OCT-2003; 2003US-0510318P.
 XX 07-NOV-2003; 2003US-0518453P.
 XX (ALNY-) ALNYLAM PHARM.
 XX Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX Example 5; SEQ ID NO 4395; 378pp; English.
 XX The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (MI) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart

CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
 CC can be used to control ApoB gene expression.
 XX Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 63.2%; Score 15.8; DB 13; Length 19;
 Best Local Similarity 57.9%; Pred. No. 1.2e+03;
 Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 3 ACUCAGGAUCCAGAUU 21
 Db ||::||| |::|||::|||:
 19 ACTTCAAGTTCAGATAT 1
 RESULT 6
 ADR77241/C
 ID ADR77241 standard; DNA; 19 BP.
 XX AC ADR77241;
 XX DT 16-DEC-2004 (first entry)
 XX DE Human apolipoprotein B (ApoB) oligonucleotide seqid 1726.
 XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
 XX OS Homo sapiens.
 XX WO2004080406-A2.
 XX 23-SEP-2004.
 XX 08-MAR-2004; 2004WO-US007070.
 XX 07-MAR-2003; 2003US-0452682P.
 XX 12-MAR-2003; 2003US-0454265P.
 XX 13-MAR-2003; 2003US-0454962P.
 XX 13-MAR-2003; 2003US-0455050P.
 XX 14-APR-2003; 2003US-0462894P.
 XX 17-APR-2003; 2003US-0463772P.
 XX 25-APR-2003; 2003US-0465665P.
 XX 25-APR-2003; 2003US-0465802P.
 XX 09-MAY-2003; 2003US-0469612P.
 XX 08-AUG-2003; 2003US-0493986P.
 XX 11-AUG-2003; 2003US-0494597P.
 XX 26-SEP-2003; 2003US-0506341P.
 XX 09-OCT-2003; 2003US-0510246P.
 XX 10-OCT-2003; 2003US-0510318P.
 XX 07-NOV-2003; 2003US-0518453P.
 XX (ALNY-) ALNYLAM PHARM.
 XX Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX Example 5; SEQ ID NO 4395; 378pp; English.
 XX The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (MI) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart

XX	Example 5; SEQ ID NO 1726; 378pp; English.	
XX	The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-O alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (MI) apob-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. (MI) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apob-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant hypercholesterolaemia, coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.	
XX	Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;	
XX	Query Match 63.2%; Score 15.8; DB 13; Length 19;	
XX	Best Local Similarity 57.9%; Pred. No. 1.2e+03;	
XX	Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	
QY	3 ACUUCAGGAUUCACAGAU 21	
DB	19 ACTTCAGGTTCCAGATAT 1	
XX	RESULT 7	
XX	ADR80185/C	
XX	ID ADR80185 standard; DNA; 19 BP.	
XX	AC ADR80185;	
XX	AC ADR80185;	
XX	16-DEC-2004 (first entry)	
XX	Human apolipoprotein B (ApoB) oligonucleotide seqid 4682.	
XX	antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;	
XX	RNA interference; iRNA; antisense technology; lipid metabolism;	
XX	cholesterol imbalance; dyslipidaemia hypercholesterolaemia;	
XX	coronary artery disease; CAD; coronary heart disease; CHD;	
XX	atherosclerosis; hepatic glucose production;	
XX	glucose-metabolism-related disorder; diabetes; cancer; breast cancer;	
XX	colon cancer; lung cancer; neurological disease; Huntington disease;	
XX	spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.	
OS	Homo sapiens.	
XX	WO2004080406-A2.	
XX	23-SEP-2004.	
XX	08-MAR-2004; 2004WO-US007070.	
XX	07-MAR-2003; 2003US-0452682P.	
XX	12-MAR-2003; 2003US-0454265P.	
XX	13-MAR-2003; 2003US-0454962P.	
XX	13-MAR-2003; 2003US-0455050P.	
XX	14-APR-2003; 2003US-0462894P.	
XX	17-APR-2003; 2003US-0463772P.	
XX	25-APR-2003; 2003US-0465665P.	
XX	25-APR-2003; 2003US-0465802P.	
XX	08-MAY-2003; 2003US-0469612P.	
XX	08-AUG-2003; 2003US-0493986P.	
XX	11-AUG-2003; 2003US-0494597P.	
XX	26-SEP-2003; 2003US-0506341P.	
XX	09-OCT-2003; 2003US-0510246P.	
XX	10-OCT-2003; 2003US-0510318P.	
XX	07-NOV-2003; 2003US-0518453P.	
XX	(ALNY-) ALNYLAM PHARM.	
XX	Manoharan M, Bumcrot D;	
XX	WPI; 2004-677362/66.	
XX	Interference RNA agent useful for treating dyslipidemias, coronary artery disease, diabetes, cancer or neurological disease, comprises sense sequence and antisense sequence which has specific modifications.	
XX	Example 5; SEQ ID NO 4682; 378pp; English.	
XX	The invention describes a RNA interference (iRNA) agent (I) comprising a sense sequence and an antisense sequence, where the sense sequences have one or more asymmetrical 2'-O alkyl modifications, the antisense sequences have one or more asymmetrical phosphorothioate modifications and the antisense sequence targets a human gene sequence. Also described are: a pharmaceutical preparation comprising (I); reducing (MI) apob-100 levels or glucose-6-phosphatase levels in a subject; producing (I); stabilising (I), involves selecting a sequence with activity and introducing one or more asymmetrical modification in the sequence, where the modification decreases nuclease sensitivity while not decreasing its activity; a kit comprising (I) and instruction for its use; and a device that can be dispense or administer a composition comprising (I). (I) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. (MI) is useful for reducing apob-100 levels or glucose-6-phosphatase levels. The subject is suffering from a disorder characterised by elevated or otherwise unwanted expression of apob-100, elevated or otherwise unwanted levels of cholesterol, and/or dysregulation of lipid metabolism. The disorder is chosen from the HDL/LDL cholesterol imbalance, dyslipidaemias, hypercholesterolaemia, statin-resistant hypercholesterolaemia, coronary artery disease (CAD), coronary heart disease (CHD) and atherosclerosis. (I) is administered to a subject to inhibit hepatic glucose production or for treating glucose-metabolism-related disorder e.g. diabetes or type-2 diabetes. (I) is useful for treating the diseases as mentioned above, cancer (e.g. breast, colon or lung cancer), neurological disease (e.g., Huntington disease or spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence represents a human apolipoprotein B (ApoB) antisense oligonucleotide that can be used to control ApoB gene expression.	
XX	Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;	
XX	Query Match 63.2%; Score 15.8; DB 13; Length 19;	
XX	Best Local Similarity 57.9%; Pred. No. 1.2e+03;	
XX	Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;	
QY	3 ACUUCAGGAUUCACAGAU 21	
DB	19 ACTTCAGGTTCCAGATAT 1	
XX	RESULT 8	
XX	ADR76955/C	
XX	ID ADR76955 standard; DNA; 19 BP.	
XX	AC ADR76955;	
XX	16-DEC-2004 (first entry)	
XX	antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;	
XX	RNA interference; iRNA; antisense technology; lipid metabolism;	
XX	cholesterol imbalance; dyslipidaemia hypercholesterolaemia;	
XX	coronary artery disease; CAD; coronary heart disease; CHD;	
XX	atherosclerosis; hepatic glucose production;	
XX	glucose-metabolism-related disorder; diabetes; cancer; breast cancer;	
XX	colon cancer; lung cancer; neurological disease; Huntington disease;	
XX	spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apob; ss.	
OS	Homo sapiens.	
XX	WO2004080406-A2.	
XX	23-SEP-2004.	
XX	08-MAR-2004; 2004WO-US007070.	
XX	07-MAR-2003; 2003US-0452682P.	
XX	12-MAR-2003; 2003US-0454265P.	
XX	13-MAR-2003; 2003US-0454962P.	
XX	13-MAR-2003; 2003US-0455050P.	
XX	14-APR-2003; 2003US-0462894P.	
XX	17-APR-2003; 2003US-0463772P.	
XX	25-APR-2003; 2003US-0465665P.	
XX	25-APR-2003; 2003US-0465802P.	
XX	08-MAY-2003; 2003US-0469612P.	
XX	08-AUG-2003; 2003US-0493986P.	
XX	11-AUG-2003; 2003US-0494597P.	

XX Human apolipoprotein B (ApoB) oligonucleotide seqid 1440.

DE antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;

XX cytosatic; anticonvulsant; nootropic; muscular; anti-HIV;

KW RNA interference; iRNA; antisense technology; lipid metabolism;

KW cholesterol imbalance; dyslipidemia hypercholesterolaemia;

KW coronary artery disease; CAD; coronary heart disease; CHD;

KW atherosclerosis; hepatic glucose production;

KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;

KW colon cancer; lung cancer; neurological disease; Huntington disease;

KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.

OS Homo sapiens.

XX WO2004080406-A2.

PN 23-SEP-2004.

XX 08-MAR-2004; 2004WO-US007070.

XX 07-MAR-2003; 2003US-0452682P.

PR 12-MAR-2003; 2003US-0454265P.

PR 13-MAR-2003; 2003US-0454962P.

PR 13-MAR-2003; 2003US-0455050P.

PR 14-APR-2003; 2003US-0462894P.

PR 17-APR-2003; 2003US-0463772P.

PR 25-APR-2003; 2003US-0465665P.

PR 25-APR-2003; 2003US-0465802P.

PR 09-MAY-2003; 2003US-0469612P.

PR 08-AUG-2003; 2003US-0493986P.

PR 11-AUG-2003; 2003US-0494597P.

PR 26-SEP-2003; 2003US-0506341P.

PR 09-OCT-2003; 2003US-0510246P.

PR 10-OCT-2003; 2003US-0510318P.

PR 07-NOV-2003; 2003US-0518453P.

XX (ALNY-) ALNYLAM PHARM.

XX Manoharan M, Bumcrot D;

XX WPI; 2004-677362/66.

XX Interference RNA agent useful for treating dyslipidemias, coronary artery

PT disease, diabetes, cancer or neurological disease, comprises sense

PT sequence and antisense sequence which has specific modifications.

XX Example 5; SEQ ID NO 1440; 378pp; English.

XX The invention describes a RNA interference (iRNA) agent (I) comprising a

CC sense sequence and an antisense sequence, where the sense sequences have

CC one or more asymmetrical 2'-O alkyl modifications, the antisense

CC sequences have one or more asymmetrical phosphorothioate modifications

CC and the antisense sequence targets a human gene sequence. Also described

CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100

CC levels or glucose-6-phosphatase levels in a subject; producing (I);

CC stabilising (I), involves selecting a sequence with activity and

CC introducing one or more asymmetrical modification in the sequence, where

CC the modification decreases nuclease sensitivity while not decreasing its

CC activity; a kit comprising (I) and instruction for its use; and a device

CC that can be dispense or administer a composition comprising (I). (I) is

CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)

CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.

CC The subject is suffering from a disorder characterised by elevated or

CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted

CC levels of cholesterol, and/or dysregulation of lipid metabolism. The

CC disorder is chosen from the HDL/LDL cholesterol imbalance,

CC dyslipidaemias, hypercholesterolaemia, statin-resistant

CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart

CC disease (CHD) and atherosclerosis. (I) is administered to a subject to

CC inhibit hepatic glucose production or for treating glucose-metabolism-

CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for

CC treating the diseases as mentioned above, cancer (e.g. breast, colon or

CC lung cancer), neurological disease (e.g., Huntington disease or

CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence

CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that

CC can be used to control ApoB gene expression.

XX Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

SQ Sequence 19; Length 19;

Query Match 63.2%; Score 15.8; DB 13;

Best Local Similarity 57.9%; Pred. No. 1.2e+03;

Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ACUUCAGGAUUCAGAUU 21

Db 19 ACTTCAAGGTTCCAGATAT 1

RESULT 9

AAD48330

ID AAD48330 standard; DNA; 20 BP.

XX AAD48330;

AC AAD48330;

XX 24-FEB-2003 (first entry)

DT Apo B3500 DNA amplifying reverse PCR primer.

DE Single nucleotide polymorphism; SNP; antisense therapy; viral infection;

XX PCR; primer; ss.

KW Unidentified.

OS EP1247815-A2.

XX 09-OCT-2002.

PD 25-MAR-2002; 2002EP-00388025.

XX 25-MAR-2001; 2001US-0278598P.

XX (EXIQ-) EXIQON AS.

PA Jakobson MH, Kongsbak L, Pfundheller H;

PI WPI; 2003-042042/04.

XX Chimeric oligonucleotide useful as primer in nucleic acid extension and

PT amplification reactions and as capture probe in single nucleotide

PT polymorphism assays, has non-modified and modified nucleic acid residues.

XX Example 1; Page 9; 12pp; English.

XX The invention relates to chimeric oligonucleotide containing modified and

CC non-modified nucleic acid residues which are useful as primer in nucleic

CC acid extension and amplification reactions and as capture probe in single

CC nucleotide polymorphism (SNP) assays. Multiple primers are used in

CC multiplex PCR. The invention is useful in diagnostic purposes, as probes

CC in the purification, isolation and detection of pathogenic organisms such

CC as virus, bacteria or fungi, as generic tools for purification,

CC isolation, amplification and detection of nucleic acids from groups of

CC related species such as for instance RNA from gram- positive or gram

CC negative bacteria, fungi, mammalian cells. It is also useful as an

CC aptamer in molecular diagnostic e.g. in RNA mediated catalytic processes,

CC in specific binding of antibiotics, drugs, amino acids, peptides,

CC structural proteins, protein receptors, saccharides, enzymes,

CC polysaccharides, biological cofactors, nucleic acids, or triphosphates or

CC in the separation of enantiomers from racemic mixtures by stereospecific

CC binding. It is also used in antisense therapy for treating diseases e.g.

CC viral infection. The present sequence is a PCR primer used for amplifying

CC Apo B3500 DNA. This sequence is used in the exemplification of the

XX invention

SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

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Query Match      63.2%; Score 15.8; DB 10; Length 20;
Best Local Similarity 57.9%; Pred. No. 1.2e+03;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACUCAGGAUCCAGAUU 21
Db 1 ACTTCAAGGTTCCAGATAT 19

RESULT 10
AAQ10823/c
ID AAQ10823 standard; DNA; 34 BP.
XX
XX AAQ10823;
AC
XX
XX 09-MAY-1991 (first entry)
DT
XX
DE Pneumocystis carinii 18S rRNA-targeted probe, 1485.
XX
XX Hybridisation assay; pneumonia; AIDS; ss.
XX
XX Synthetic.
XX
XX WO9102092-A.
XX
XX 21-FEB-1991.
XX
XX 11-AUG-1989; 89US-00392679.
XX
XX 11-AUG-1989; 89US-00392679.
XX
XX (GENE-) GENE-TRAK SYST.
PA
XX
XX Shah JS, Buharin A, Lane DJ;
PI
XX WPI; 1991-073563/10.
DR
XX
XX Nucleic acid fragment - capable of hybridising to r RNA or r DNA of
PT pneumocystis carinii, useful as probes for detection of P carinii.
XX
XX Disclosure; Page 11; 36pp; English.
PS
XX
XX This oligonucleotide has a sequence specific for a region of the rDNA of
CC Pneumocystis carinii, the causative agent of pneumonia. It can be used as
CC a probe in hybridisation assays to detect P. carinii in clinical samples.
CC This probe detects human but not most non-human P. carinii isolates. See
CC also AAQ10820-22 and AAQ10824-33
XX
XX Sequence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;

Query Match      62.4%; Score 15.6; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUUCCCC 25
Db 26 CTCTGGATTACCGGTATGCC 5

RESULT 11
AAT42447/c
ID AAT42447 standard; DNA; 34 BP.
XX
XX AAT42447;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 08-JAN-1997 (first entry)
DT
XX
DE Probe 1485 for P. carinii 18S rRNA.
XX
XX Probe; pneumocystis carinii; 18S rRNA; human; mammal; immunodeficiency;
KW pneumonia; ferret; rat; ss.
XX
XX

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OS Synthetic.
XX US5519127-A.
PN
XX
XX 21-MAY-1996.
PD
XX
XX 21-JAN-1992; 92US-00826657.
PF
XX
XX 11-AUG-1989; 89US-00392679.
PR
XX
XX (STAD ) AMOCO CORP.
PA
XX
XX Lane DJ, Buharin A, Shah J;
PI
XX WPI; 1996-259122/26.
DR
XX
XX Nucleic acid probes specific for human Pneumocystis carinii - provide
PT sensitive, accurate and rapid diagnosis of infection.
XX
XX Claim 1; Col 13-14; 15pp; English.
PS
XX
XX AAT42443-742456 represent probes for human Pneumocystis carinii (Pc) 18S
CC rRNA. Pc infects humans and most mammalian hosts, but rarely cause
CC illness in normal individuals. However, in certain conditions of
CC immunodeficiency, Pc does give rise to life threatening pneumonia. This
CC sequence hybridises to the 18S rRNA at positions 641-652, and is capable
CC of hybridisation to human Pc. These probes can be used as a probe set for
CC a Pc assay. The 1485 (this sequence), 1487 (see AAT42452) and 1159 (see
CC AAT42448) probes are reactive with all human Pc isolates. The probes 1485
CC and 1487 hybridise to rRNA and rDNA of human Pc, but not to other fungi
CC or bacteria. The 1485 and 1487 probes can therefore be used to detect Pc
CC in clinical samples. The rest of these probe sequences are reactive
CC mainly with ferret Pc and non-human strains of Pc. By using these probe
CC sequences, a more sensitive, accurate and rapid diagnosis can be
CC performed, with reduced expense, in comparison to current technology.
CC rRNA is present in the cell at high concentration, and is not likely to
CC undergo lateral transfer. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 34 BP; 12 A; 7 C; 11 G; 4 T; 0 U; 0 Other;

Query Match      62.4%; Score 15.6; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUUCCCC 25
Db 26 CTCTGGATTACCGGTATGCC 5

RESULT 12
ABL40079/c
ID ABL40079 standard; DNA; 41 BP.
XX
XX ABL40079;
AC
XX
XX 15-MAY-2002 (first entry)
DT
XX
XX Phosphoenolpyruvate-dependent sugar phosphotransferase 12 probe 2.
DE
XX
XX Human; phosphoenolpyruvate-dependent sugar phosphotransferase 12; enzyme;
KW cytosolic; haemostatic; virucide; immunomodulatory; haemopathy;
KW antiinflammatory; gene therapy; malignant tumour; HIV infection;
KW human immunodeficiency virus infection; immunological disease;
KW inflammation; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200200830-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 11-JUN-2001; 2001WO-CN000950.
XX
XX

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CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
 Query Match 60.0%; Score 15; DB 4; Length 17;
 Best Local Similarity 73.3%; Pred. No. 2.9e+03;
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 11 AUUCCAGAUAGGCC 25
 Db 17 ATTCCAGATATGCC 3
 RESULT 15
 ABK01442/c
 ID ABK01442 standard; RNA; 17 BP.
 XX
 AC ABK01442;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #712.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;

XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 89; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 60.0%; Score 15; DB 4; Length 17;
 Best Local Similarity 73.3%; Pred. No. 2.9e+03;
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 10 GAUUCAGAUAGGCC 24
 Db 15 GATTCAGATATGCC 1
 Search completed: July 30, 2005, 15:45:02
 Job time : 309.77 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:01:12 ; Search time 2428.72 Seconds
(without alignments)
391.815 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacuucaggaucaggauagccc 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.4	61.6	53	1	AU258136
C 2	15	60.0	40	8	AQ072891 EP(2)2087
C 3	14.8	59.2	34	9	TA163C01P
C 4	14	56.0	51	8	AZ836163 2M0130E20
C 5	13.6	54.4	45	9	BX532189 Arabidops
C 6	13.6	54.4	47	9	BX532135 Arabidops
C 7	13.6	54.4	50	1	AI819158 wJ94c07.x
C 8	13.6	54.4	53	9	BX530982 Arabidops
C 9	13.6	54.4	55	2	AW156165 se20d03.y
C 10	13.6	54.4	59	9	BX532084 Arabidops
C 11	13.6	54.4	59	9	BX532497 Arabidops
C 12	13.4	53.6	28	1	AI025442 ov57d04.x
C 13	13.4	53.6	29	1	AJ658580 Arabidops
C 14	13.4	53.6	51	9	CR110498 Forward s
C 15	13.4	53.6	60	4	BM360861 8 cDNA su
C 16	13.2	52.8	34	9	AG198942 Pan trogl
C 17	13.2	52.8	39	9	BX532083 Arabidops
C 18	13.2	52.8	53	5	BM893982 Arabidops
C 19	13.2	52.8	53	9	BX531143 Arabidops
C 20	13.2	52.8	57	9	BX532161 Arabidops
C 21	13.2	52.8	59	8	BH803246 Arabidops
C 22	13.2	52.8	60	7	CR579578 Arabidops
C 23	13	52.0	51	8	AZ598697 Arabidops
C 24	13	52.0	51	8	BZ593237 SALK_0682

25	13	52.0	52	7	CR415880	CR415880 CR415880
C 26	13	52.0	58	7	R71713	R71713 yJ85f02.r1
C 27	12.8	51.2	48	9	CL529721	CL529721 HIV36E3.Y
C 28	12.8	51.2	52	2	BE320905	BE320905 NF028B03R
C 29	12.8	51.2	53	6	C20879	C20879 HUMGS000494
C 30	12.8	51.2	60	8	BH855668	BH855668 SALK_0848
C 31	12.6	50.4	43	1	AA780094	AA780094 af36509.s
C 32	12.6	50.4	43	9	CR403886	CR403886 Arabidops
C 33	12.6	50.4	53	9	CR233626	CR233626 Forward s
C 34	12.6	50.4	55	1	AI583015	AI583015 tr99c12.x
C 35	12.6	50.4	59	8	BZ764153	BZ764153 SALK_1240
C 36	12.4	49.6	35	8	AZ345880	AZ345880 IM0080013
C 37	12.4	49.6	38	8	AZ974759	AZ974759 2M0249P02
C 38	12.4	49.6	49	9	AL768749	AL768749 Arabidops
C 39	12.4	49.6	50	1	AU104145	AU104145 Arabidops
C 40	12.4	49.6	50	1	AU107193	AU107193 Arabidops
C 41	12.4	49.6	50	8	BZ765214	BZ765214 SALK_1293
C 42	12.4	49.6	52	8	AZ449667	AZ449667 IM0248E05
C 43	12.4	49.6	52	8	AZ595018	AZ595018 IM0407C22
C 44	12.4	49.6	54	9	BX659005	BX659005 Arabidops
C 45	12.4	49.6	56	1	AA667054	AA667054 vq88c02.r

ALIGNMENTS

RESULT 1
LOCUS AU258136/c 53 bp mRNA linear EST 25-APR-2002
DEFINITION AU258136 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0012210 3', mRNA sequence.
ACCESSION AU258136
VERSION AU258136.1 GI:20323426
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 53)
AUTHORS Kato, K. and Matoba, R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 530-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkat@bs.aist-nara.ac.jp/
URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

source

1..53
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0012210"
/issue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 61.6%; Score 15.4; DB 1; Length 53;
Best Local Similarity 58.8%; Pred. No. 2.1e+04;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 UUCAGGAUCCAGAU 21

DB 52 TTCAGGGTCCAGATAT 36

RESULT 2

AQ072891/c 40 bp DNA linear GSS 23-AUG-2000
LOCUS AQ072891
DEFINITION EP(2)2087-Sprime Drosophila melanogaster EP line Drosophila


```

source
1. .53
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-471A05-019883"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 54.4%; Score 13.6; DB 9; Length 53;
Best Local Similarity 55.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACUACAGGAUCCAGAUU 21
||:||||:||||:|
Db 50 AGCTTGAGGATCCACATAT 31

RESULT 9
AW156165/c
LOCUS
DEFINITION
ae20d03.v1 Gm-cl015 Glycine max cdna clone GENOME SYSTEMS CLONE ID:
Gm-cl015-1758 5', mRNA sequence.
ACCESSION
AW156165
VERSION
AW156165.1 GI:6227566
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 55)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert length: 241 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .55
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl015-1758"
/tissue_type="Mature flowers, field grown plants"
/lab_host="X110-Gold"
/clone_lib="Gm-cl015"
/notes="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:

XhoI; This cdna library was constructed from mRNA isolated
from mature flowers of field grown plants. The cdna
library was prepared using the Stratagene pBluescript II
XR cdna library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(AT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cdna fragments followed by
XhoI digestion. The cdna fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cdna fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."

ORIGIN
Query Match 54.4%; Score 13.6; DB 2; Length 55;
Best Local Similarity 55.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACUUCAGGAUCCAGAUUG 22
||:||||:||||:|
Db 22 ACATTAGGTTCCAGATCTG 3

RESULT 10
BX532084/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-487A04-019572,
Genomic survey sequence.
ACCESSION
BX532084
VERSION
BX532084.1 GI:31409214
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
REFERENCE
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 59)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At5g05120.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
```


was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'.
TGTACCAATCTGAAGTGGAGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 53.6%; Score 13.4; DB 1; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 5 UUCAGGAGUCCAGAU 19

Db 21 TTCAGGATTACAGAT 7

RESULT 13

AJ658580

LOCUS

AJ658580 KN277 Sus scrofa cDNA clone C0005213_H23, mRNA sequence. EST 28-JUN-2004

ACCESSION

AJ658580

VERSION

AJ658580.1

KEYWORDS

EST.

SOURCE

Sus scrofa

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 29)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson, S.I.

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

v0.020425.c. Vector identified by cross match with the -minscore 20

and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site1: EcoRI

R. Site2: NotI 5'. Seq Primer M13f Normalised library constructed

from pooled early embryos, from 8- cell stage to blastocysts.

Clones available from UK Centre for Functional Genomics in Farm

Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,

www.arkgenomics.org.

FEATURES

Location/Qualifiers

1..29

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0005213_H23"

/tissue_type="embryo"

/clone_lib="KN277"

/notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:

NotI; Single pass sequencing. Normalised library

constructed from pooled early embryos, from 8-cell stage

to blastocysts."

ORIGIN

source

1..60

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/mol_type="mRNA"

/db_xref="taxon:9606"

/map="17"

/tissue_type="rectum"

/dev_stage="73 years old"

/clone_lib="cDNA subtractive library of human rectum

adenocarcinoma"

/note="Vector: pMD18T-vector"

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..51

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="MHPN410121"

/clone_lib="MHPN"

ORIGIN

Query Match

Best Local Similarity

Matches

13; Conservative

4; Mismatches

6; Indels

0; Gaps

0;

QY

1

CAACUUCAGAUUCCAGAUUGC

23

Db

51

CAATTGGGAAAGCAGATATGC

29

RESULT 15

BM360861

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ORIGIN

source

1..60

/organism="Homo sapiens"

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/map="17"

/tissue_type="rectum"

/dev_stage="73 years old"

/clone_lib="cDNA subtractive library of human rectum

adenocarcinoma"

/note="Vector: pMD18T-vector"

ORIGIN

source

1..60

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/map="17"

/tissue_type="rectum"

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/clone_lib="cDNA subtractive library of human rectum

adenocarcinoma"

/note="Vector: pMD18T-vector"

CR110498 51 bp DNA linear GSS 05-JUL-2004
Forward strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN410j21, genomic survey sequence.

CR110498
VERSION
GSS; genome survey sequence; MICR.

CR110498.1 GI:49857913
KEYWORDS
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 51)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ADAMS, D.J., BIGGS, P.J., COX, A.V., DAVIES, R.M., VAN DER WEYDEN, L.,
JONKERS, J., SMITH, J., PLUMB, R.W., TAYLOR, R.G., NISHIJIMA, I., YU, Y.,
ROGERS, U. and BRADLEY, A.

Direct Submision

TITLE
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

JOURNAL
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES
Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

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/clone="MHPN410j21"

/clone_lib="MHPN"

ORIGIN

Query Match 53.6%; Score 13.4; DB 9; Length 51;

Best Local Similarity 56.5%; Pred. No. 1.8e+05;

Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

0;

QY

1

CAACUUCAGAUUCCAGAUUGC

23

Db

51

CAATTGGGAAAGCAGATATGC

29

RESULT 15

BM360861

LOCUS

DEFINITION

8 cDNA subtractive library of human rectum adenocarcinoma Homo

sapiens cDNA, mRNA sequence.

ACCESSION

BM360861

VERSION

BM360861.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 60)

Chen, Y. and Zhang, Y.Z.

Expressed sequence tags from a subtracted cDNA library of human

rectum adenocarcinoma

U.S. Chin. J. Lymphology Oncol. 2 (2), 9-14 (2002)

Contact: Yao Chen

Life Science College of Sichuan University and the department of

anatomy of basic and legal medical institute of west china medical

center of Sichuan University

Chengdu, Sichuan, P.O.Box 610041, P.R.CHINA

Tel: 86 028 5501361

Email: xmxh@263.net

Insert Length: 60 Std Error: 0.00.

Location/Qualifiers

1..60

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="17"

/tissue_type="rectum"

/dev_stage="73 years old"

/clone_lib="cDNA subtractive library of human rectum

adenocarcinoma"

/note="Vector: pMD18T-vector"

ORIGIN

source

1..60

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Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AACUUCAGGAUUCACAGAUAGCC 24
|||:|||||:|:|
Db 22 AACCTCAGGATTCTCCCTCTGCC 44

Search completed: July 30, 2005, 18:20:53
Job time : 2439.72 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:05:52 ; Search time 87.8378 Seconds
(without alignments)

Title: US-09-544-776-4

Perfect score: 25
Sequence: 1 caacuaggauuccagauauqccc 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

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Minimum DB seq length: 0
Maximum DB seq length: 60
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : Issued Patents NA: *

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2: /cgm2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgm2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgm2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgm2_6/prodata/1/ina/PCTUS_COMB.seq.*
6: /cgm2_6/prodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.6	62.4	33	6	5519127-17	Patent No. 5519127
2	15.6	62.4	33	6	5519127-36	Patent No. 5519127
3	15.6	62.4	33	6	5519127-17	Patent No. 5519127
4	15.6	62.4	33	6	5519127-36	Patent No. 5519127
C 5	15.6	62.4	34	6	5519127-4	Patent No. 5519127
C 6	15.6	62.4	34	6	5519127-4	Patent No. 5519127
7	15.6	62.4	39	6	5519127-33	Patent No. 5519127
8	15.6	62.4	39	6	5519127-33	Patent No. 5519127
9	15	60.0	25	4	US-09-396-196G-88973	Sequence 88973, A
10	14.8	59.2	38	4	US-08-793-273C-22	Sequence 22, Appl
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12	14.2	56.8	25	4	US-09-396-196G-64379	Sequence 64379, A
C 13	14.2	56.8	25	4	US-09-396-196G-118281	Sequence 118281, A
C 14	14	56.0	25	4	US-09-396-196G-83713	Sequence 83713, A
C 15	14	56.0	34	6	5519127-14	Patent No. 5519127
C 16	14	56.0	39	6	5519127-34	Patent No. 5519127
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18	14	56.0	48	3	5519127-34	Patent No. 5519127
C 19	14	56.0	48	3	US-09-367-206-34	Sequence 34, Appl
C 20	13.8	55.2	25	4	US-09-396-196G-15817	Sequence 15817, A
C 21	13.8	55.2	25	4	US-09-396-196G-66465	Sequence 66465, A
C 22	13.8	55.2	27	4	US-09-958-940-7	Sequence 7, Appl
C 23	13.8	55.2	36	1	US-08-105-483-64	Sequence 64, Appl
24	13.8	55.2	36	1	US-08-709-209-64	Sequence 64, Appl
25	13.8	55.2	36	1	US-08-458-101-64	Sequence 64, Appl
26	13.8	55.2	59	3	US-09-101-751A-82	Sequence 82, Appl
C 27	13.6	54.4	25	4	US-09-827-998-1853	Sequence 1853, A

C 28	13.6	54.4	25	4	US-09-827-998-1854	Sequence 1854, Ap
C 29	13.6	54.4	25	4	US-09-827-998-1855	Sequence 1855, Ap
C 30	13.6	54.4	25	4	US-09-827-998-1856	Sequence 1856, Ap
C 31	13.6	54.4	25	4	US-09-827-998-1857	Sequence 1857, Ap
C 32	13.6	54.4	25	4	US-09-827-998-1858	Sequence 1858, Ap
C 33	13.6	54.4	25	4	US-09-396-136G-16054	Sequence 16064, A
C 34	13.6	54.4	25	4	US-09-396-136G-85548	Sequence 85548, A
C 35	13.6	54.4	30	1	US-08-499-568-12	Sequence 12, Appl
C 36	13.6	54.4	30	1	US-08-793-958-12	Sequence 12, Appl
C 37	13.6	54.4	32	1	US-09-001-157-5	Sequence 5, Appl
C 38	13.6	54.4	32	2	US-09-001-157-5	Sequence 5, Appl
C 39	13.6	54.4	47	4	US-09-423-978-2846	Sequence 2846, Ap
C 40	13.6	54.4	51	4	US-09-443-193C-845	Sequence 845, App
C 41	13.4	53.6	25	4	US-09-396-136G-42375	Sequence 42375, A
C 42	13.4	53.6	25	4	US-09-396-136G-93769	Sequence 93769, A
C 43	13.4	53.6	34	4	US-09-694-127-12	Sequence 12, Appl
C 44	13.4	53.6	35	4	US-09-362-394A-8	Sequence 8, Appl
C 45	13.4	53.6	44	3	US-09-443-501A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
5519127-17
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA, BUHARIN, AMELIA, LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 17:
; LENGTH: 33
5519127-17

Query Match	62.4%	Score 15.6;	DB 6;	Length 33;
Best Local Similarity	54.5%;	Pred. No. 3.4e+02;		
Matches 12;	Conservative	6;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy' .
4 CUUCAGGAUUC CAGAUAUGCCC 25
|::|||::| |::|||
Db
9 CTTCGGATTACCGGTATGCCC 30

RESULT 2
5519127-36
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA, BUHARIN, AMELIA, LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:36:
; LENGTH: 33
5519127-36

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Query Match      62.4%; Score 15.6; DB 6; Length 33;
Best Local Similarity 81.8%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4  CUUCAGGAUCCAGAUAGCCC 25
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Db       9  CUUCUGGAUACCGUAUGCCC 30

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RESULT 3
5519127-17
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:17:
; LENGTH: 33
5519127-17
Query Match 62.4%; Score 15.6; DB 6; Length 33;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCGAGUAUGCCC 25
Db 9 CTTCTGGATTACCGGTATGCC 30

RESULT 4
5519127-36
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:36:
; LENGTH: 33
5519127-36
Query Match 62.4%; Score 15.6; DB 6; Length 33;
Best Local Similarity 81.8%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCGAGUAUGCCC 25
Db 9 CUUCUGGAUUAACCGUAUGCCC 30

RESULT 5
5519127-4/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:4:
; LENGTH: 34
5519127-4
Query Match 62.4%; Score 15.6; DB 6; Length 34;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
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Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCGAGUAUGCCC 25
Db 26 CTTCTGGATTACCGGTATGCC 5

RESULT 6
5519127-4/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:4:
; LENGTH: 34
5519127-4
Query Match 62.4%; Score 15.6; DB 6; Length 34;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCGAGUAUGCCC 25
Db 26 CTTCTGGATTACCGGTATGCC 5

RESULT 7
5519127-33
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:33:
; LENGTH: 39
5519127-33
Query Match 62.4%; Score 15.6; DB 6; Length 39;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CUUCAGGAUUCGAGUAUGCCC 25
Db 10 CUUCUGGAUUAACCGUAUGCCC 31

RESULT 8
5519127-33
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:33:
; LENGTH: 39
5519127-33
Query Match 62.4%; Score 15.6; DB 6; Length 39;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; LENGTH: 39
5519127-33

Query Match          62.4%; Score 15.6; DB 6; Length 39;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CUUCAGGAUUCGAGUAUAGCCC 25
DB 10 CUUCAGGAUUCGAGUAUAGCCC 31

RESULT 9
US-09-396-196G-88973
; Sequence 88973, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88973

Query Match          60.0%; Score 15; DB 4; Length 25;
Best Local Similarity 56.5%; Pred. No. 6.4e+02;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 ACUUCAGGAUUCGAGUAUAGCCC 25
DB 1 ACTTCGGATTCCATTATGCCC 23

RESULT 10
US-08-793-273C-22
; Sequence 22, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME
; FILE REFERENCE: BEC0022S
; CURRENT APPLICATION NUMBER: US/08/793,273C
; CURRENT FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: 08/308,359
; PRIOR FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-793-273C-22

Query Match          59.2%; Score 14.8; DB 4; Length 38;
Best Local Similarity 61.1%; Pred. No. 8.6e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 UUCAGGAUUCGAGUAUAG 22
DB 14 TTCAGAAATTCAGAAATG 31

RESULT 11
PCT-US95-11684-22
; Sequence 22, Application PC/TUS9511684
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
; TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11684
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,359
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: BEC0019P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-11684-22

Query Match          59.2%; Score 14.8; DB 5; Length 38;
Best Local Similarity 61.1%; Pred. No. 8.6e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 UUCAGGAUUCGAGUAUAG 22
DB 14 TTCAGAAATTCAGAAATG 31

RESULT 12
US-09-396-196G-64379
; Sequence 64379, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-64379

Query Match      56.8%; Score 14.2; DB 4; Length 25;
Best Local Similarity 57.9%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAG 22
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Db 6 CTACAGCATTCACGATG 24

RESULT 13
US-09-396-196G-118281/c
; Sequence 118281, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118281
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-118281

Query Match      56.8%; Score 14.2; DB 4; Length 25;
Best Local Similarity 63.2%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAG 22
   ||| ||| ||| ||| |||
Db 24 CTCAGGACTCCAGGAATG 6

RESULT 14
US-09-396-196G-83713/c
; Sequence 83713, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
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US-09-396-196G-83713

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAG 22
   ||| ||| ||| ||| |||
Db 22 CATCTTCAAGTTCTCTGATGTG 1

RESULT 15
5519127-14/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA,BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:14:
; LENGTH: 34
5519127-14

Query Match      56.0%; Score 14; DB 6; Length 34;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 CUUCAGGAUCCAGAUAGCCC 25
   ||| ||| ||| ||| |||
Db 26 CTTCGGATTACCAATATGCTC 5

Search completed: July 30, 2005, 18:25:12
Job time : 87.8378 secs
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:54:37 ; Search time 689.514 Seconds
(without alignments)
1686.588 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	17	70.8	17	6	AX216092 Sequence
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C 6	16	66.7	17	6	AX216090 Sequence
C 7	16	66.7	17	6	AX217252 Sequence
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9	15.4	64.2	60	6	CQ537206 Sequence
10	15.2	63.3	51	6	CQ001884 Sequence
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C 12	15	62.5	17	6	AX216640 Sequence
13	14.6	60.8	32	6	AR217875 Sequence
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15	14.2	59.2	23	6	CQ809740 Sequence
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17	14.2	59.2	24	6	I64421 Sequence 43
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20	14.2	59.2	32	6	BD094992	BD094992 Apoptosis
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C 22	14	58.3	33	6	AX317513	AX317513 Sequence
23	14	58.3	46	6	AI17061	AI17061 oligonucleo
24	14	58.3	46	6	I11879	I11879 Sequence 45
C 25	14	58.3	60	6	CQ536100	CQ536100 Sequence
26	14	58.3	60	6	CQ538479	CQ538479 Sequence
C 27	13.8	57.5	20	6	AR075704	AR075704 Sequence
C 28	13.8	57.5	20	6	I85582	I85582 Sequence 3
29	13.8	57.5	20	6	AR307896	AR307896 Sequence
C 30	13.8	57.5	22	6	AX497015	AX497015 Sequence
C 31	13.8	57.5	23	6	BD259944	BD259944 LIM miner
C 32	13.8	57.5	23	6	AR227706	AR227706 Sequence
C 33	13.8	57.5	23	6	AR282708	AR282708 Sequence
C 34	13.8	57.5	23	6	AR369800	AR369800 Sequence
C 35	13.8	57.5	23	6	BD073527	BD073527 Novel bon
C 36	13.8	57.5	33	6	AR369001	AR369001 Sequence
C 37	13.8	57.5	33	6	BD011033	BD011033 HIV probe
38	13.6	56.7	25	6	A47542	A47542 Sequence 37
39	13.6	56.7	25	6	AR097953	AR097953 Sequence
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41	13.6	56.7	30	6	BD168952	BD168952 Drug resi
42	13.6	56.7	30	6	I13289	I13289 Sequence 9
C 43	13.6	56.7	51	6	AX116789	AX116789 Sequence
C 44	13.6	56.7	60	6	CQ547591	CQ547591 Sequence
C 45	13.6	56.7	60	6	CQ548554	CQ548554 Sequence

ALIGNMENTS

RESULT 1
AX216091/c
LOCUS AX216091 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1533 from Patent WO0159103.
ACCESSION AX216091
VERSION AX216091.1 GI:15526134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1533 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 3 UCCACCAGGCGCCAGCA 19
Db 17 TCCACCAGTGCCTCAGA 1
RESULT 2
AX216092/c
LOCUS AX216092 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1534 from Patent WO0159103.
ACCESSION AX216092
VERSION AX216092.1 GI:15526135
KEYWORDS synthetic construct
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1534 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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1. .17
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Best Local Similarity 76.5%; Pred. No. 1e+04;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACGAGGCUCA 17
Db 17 ATTCCACGAGTGCCTCA 1
RESULT 3
AX216332/c
LOCUS AX216332 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1774 from Patent W00159103.
ACCESSION AX216332
VERSION AX216332.1 GI:15526393
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1774 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 8 CAGUGCCUCAGUAGGA 24
Db 17 CAGTGCCTCAGATAGGA 1
RESULT 4
AX216639/c
LOCUS AX216639 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2081 from Patent W00159103.
ACCESSION AX216639
VERSION AX216639.1 GI:15526700
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL nogo gene expression
Patent: WO 0159103-A 2081 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 70.8%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 CACCAGUGCCUCAGAU 21
Db 17 CACCAGTGCCTCAGATA 1
RESULT 5
AX217251/c
LOCUS AX217251 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2693 from Patent W00159103.
ACCESSION AX217251
VERSION AX217251.1 GI:15527312
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2693 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
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Best Local Similarity 82.4%; Pred. No. 1e+04;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACCAGUGCCUCAGAUAG 22
Db 17 ACCAGTGCCTCAGATAG 1
RESULT 6
AX216090/c
LOCUS AX216090 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1532 from Patent W00159103.
ACCESSION AX216090
VERSION AX216090.1 GI:15526133
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1532 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers


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source
1. 17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 66.7%; Score 16; DB 6; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.1e+04;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AGUGCCUCAGAUAGGA 24
||:||||:||||:||||
Db 17 AGTGCCTCAGATAGGA 2

RESULT 7
LOCUS AX217252/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2694 from Patent WO0159103.
ACCESSION AX217252
VERSION AX217252.1 GI:15527313
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J., and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2694 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 66.7%; Score 16; DB 6; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.1e+04;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUUCCACGAGGCTC 16
||:||||:||||:|
Db 16 ATCCACGAGTGCCTC 1

RESULT 8
LOCUS AF200461 60 bp mRNA linear PRI 01-MAR-2000
DEFINITION Homo sapiens T-cell receptor beta mRNA, partial cds.
ACCESSION AF200461
VERSION AF200461.1 GI:7110211
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 60)
JOURNAL Pachman, L. M., Liotta, M. R., Lawton, T., Morello, P., Pope, R. M.,
New Onset Juvenile Dermatomyositis: Evidence of Vbetas T cell
Receptor Oligoclonality in Muscle Biopsies of DQAI*0501 Caucasian
Children
REFERENCE 2
AUTHORS (bases 1 to 60)
Pachman, L. M., Liotta, M. R., Lawton, T., Morello, P., Pope, R. M.,
Wu, T. T. and Concannon, P.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-1999) Immunology, Children's Memorial Institute

for Education and Research (CMIER), 2430 N. Halsted, Chicago, IL
60614, USA
FEATURES
source
1. 60
/organism="Homo sapiens"
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/isoLate="patient 133"
/db_xref="taxon:9606"
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/tissue type="muscle"
/note="Isolated from patient with untreated recent onset
juvenile dermatomyositis"
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ORIGIN
Query Match 65.0%; Score 15.6; DB 9; Length 60;
Best Local Similarity 63.6%; Pred. No. 3.7e+04;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 UUCCACGAGCCUCAGAUAGG 23
:||||:||||:|
Db 13 TGCCAGCAGTTCCTCATATAGG 34

RESULT 9
LOCUS CQ537206 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6841 from Patent WO0210449.
ACCESSION CQ537206
VERSION CQ537206.1 GI:41503470
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Paigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 6841 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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1. 60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 64.2%; Score 15.4; DB 6; Length 60;
Best Local Similarity 76.5%; Pred. No. 4.6e+04;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACCAGUGCCUCAGAUAG 22
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Db 2 ACCAGTGCCTCAGGTAG 18

RESULT 10
LOCUS CQ001884 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 524 from Patent WO0147944.
ACCESSION CQ001884
VERSION CQ001884.1 GI:41008516
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1
TITLE Shinketsu, R.A. and Leach, M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0147944-A 524 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43948635"
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Best Local Similarity 70.0%; Pred. No. 5.9e+04;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 UCCACGAGGCGCUCAGAUAG 22
Db 18 TCCGTCAGTGCCTCAGACAG 37
RESULT 11
AX215272/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 714 from Patent WO0159103.
ACCESSION AX215272
VERSION AX215272.1 GI:15525315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 714 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
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/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 62.5%; Score 15; DB 6; Length 17;
Best Local Similarity 80.0%; Pred. No. 9.1e+04;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 10 GUGCCUCAGAUAGGA 24
Db 17 GTGCCTCAGTAGGA 3
RESULT 12
AX216640/c 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 2082 from Patent WO0159103.
ACCESSION AX216640
VERSION AX216640.1 GI:15526701
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 2082 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 73.3%; Pred. No. 9.1e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUUCCACCAGGCGCU 15
Db 15 ATTCCACCAGTGCCT 1
RESULT 13
AR217875 32 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 12 from patent US 6417002.
ACCESSION AR217875
VERSION AR217875.1 GI:23317769
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Horlick, R.A. and Chelsky, D.
TITLE Method for maintenance and selection of episomes
JOURNAL Patent: US 6417002-A 12 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
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Best Local Similarity 61.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 3 UCCACGAGGCGCUCAGAUAGG 23
Db 12 TTCACCTTGTGGCTCAGATAGG 32
RESULT 14
CQ550946 60 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 20581 from Patent WO0210449.
ACCESSION CQ550946
VERSION CQ550946.1 GI:41517373
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 20581 07-FEB-2002;
CompuGen Inc. (US)
FEATURES Location/Qualifiers
source 1..60
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match      60.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity 58.3%; Pred.No. 1.4e+05;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24
   ||| ||| ||| ||| ||| |||
Db 36 ATTCCCTCAGTCATCAAAATGGA 59

RESULT 15
CQ809740
LOCUS      23 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 4 from Patent WO2004035787.
ACCESSION  CQ809740
VERSION    CQ809740.1 GI:47115115
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Burcin,M., Esser,S. and Ruediger,M.
TITLE      Transplantable cell
JOURNAL    Patent: WO 2004035787-A 4 29-APR-2004;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="Primer"

ORIGIN

Query Match      59.2%; Score 14.2; DB 6; Length 23;
Best Local Similarity 57.9%; Pred.No. 2e+05;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 UUCCACCAGUGCCUCAGAU 20
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Db 3 TTCCTCCAGTTCCTCACAT 21
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Search completed: July 30, 2005, 16:20:41
Job time : 690.514 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	17	70.8	17	4	ABK02693	Human NOG
C 4	17	70.8	17	4	ABK01533	Human NOG
C 5	17	70.8	17	4	ABK01534	Human NOG
C 6	17	70.8	17	4	ABK02081	Human NOG
C 7	17	70.8	17	4	ABK01774	Human NOG
C 8	17	70.8	25	12	ADP17626	Renal cel
C 9	16	66.7	17	4	ABK01532	Human NOG
C 10	16	66.7	17	4	ABK02694	Human NOG
C 11	15.6	65.0	22	12	ADP48303	Human lym
C 12	15.6	65.0	30	2	AAV05323	PCR prime
C 13	15.4	64.2	30	6	ABS68889	Human Rec
C 14	15.4	64.2	60	6	ABN34093	Human spl
C 15	15.2	63.3	51	4	AAL27316	Human SNP
C 16	15	62.5	17	4	ABK02082	Human NOG
C 17	15	62.5	17	4	ABK00714	Human NOG
C 18	15	62.5	50	6	ABZ00669	Human leu
C 19	14.6	60.8	25	9	ACI32957	Human mic
C 20	14.4	60.0	46	3	AAA29906	Promoter

PS Claim 25; Page 32; 68pp; English.

XX The present invention describes a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can: regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides. The present sequence represents a human Nogo B

CC phosphorothioate antisense oligonucleotide from the present invention

XX

SQ Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAGGA 24

|||||

DB 1 AUUCCACCAGUGCCUCAGAUAGGA 24

|||||

RESULT 2

ID ADP17627/c

XX ADP17627 standard; DNA; 25 BP.

AC ADP17627;

XX

DT 26-AUG-2004 (first entry)

XX

DE Renal cell carcinoma differentially expressed gene probe #4032.

DE ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression; probe.

XX

OS Homo sapiens.

XX

PN WO2004048933-A2.

XX

PD 10-JUN-2004.

XX

XX 21-NOV-2003; 2003WO-US037481.

PF

XX 21-NOV-2002; 2002US-0427982P.

PR

XX 03-APR-2003; 2003US-0459782P.

XX

(AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STON/) STOVER J A.

PA (SLON/) SLONI D K.

XX

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

PI WPI; 2004-460799/43.

DR

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX

PS Disclosure; SEQ ID NO 4363; 350pp; English.

XX

XX The invention relate to a method of diagnosing (M1) non-blood disease

CC such as solid tumor by providing peripheral blood sample of human having

CC

CC non-blood disease, and comparing an expression profile of specific genes

CC in the peripheral blood sample to reference expression profile of the

CC genes, where each of the genes is differentially expressed in peripheral

CC blood mononuclear cells (PBMCs) of patients having the disease as

CC compared to PBMCs of normal humans. The method is useful for diagnosing

CC non-blood disease such as solid tumor. The solid tumor is chosen from

CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The

CC peripheral blood sample comprises enriched PBMCs. The peripheral blood

CC sample is a whole blood sample (claimed). (M1) is useful for identifying

CC genes that are differentially expressed in peripheral blood samples

CC isolated at different stages of progression, development or treatment of

CC RCC and/or other solid tumors. This sequence corresponds to a probe to

CC detect a gene that is differentially expressed and detected by the method

CC of the invention.

XX

SQ Sequence 25 BP; 8 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 91.7%; Score 22; DB 12; Length 25;

Best Local Similarity 77.3%; Pred. No. 1.1;

Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUCAGAUAG 22

|||||

DB 22 AFTCCACCAGTGCCTCAGATAG 1

|||||

RESULT 3

ABK02693/c

ID ABK02693 standard; RNA; 17 BP.

XX

AC ABK02693;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human Nogo Amberzyme #365.

XX

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; Nogo; hammerhead ribozyme;

KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200159103-A2.

XX

PD 16-AUG-2001.

XX

XX 09-FEB-2001; 2001WO-US004273.

PF

XX 11-FEB-2000; 2000US-0181797P.

PR

XX 28-FEB-2000; 2000US-0185516P.

PR

XX 06-MAR-2000; 2000US-0187128P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

XX Blatt L, Mcswiggen J, Chowrira BM;

PI

XX WPI; 2001-607195/69.

XX

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT

CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zynzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 70.8%; Score 17; DB 4; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.7e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CACGAGGCTCAGAUUA 21
 |||||:||||:||||:
 DB 17 CACGAGGCTCAGATA 1
 RESULT 7
 ID ABK01774 standard; RNA; 17 BP.
 AC ABK01774;
 DT 12-MAR-2002 (first entry)
 XX Human NOGO Zynzyme #96.
 DE
 KW Human; as; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX

PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 XX 06-MAR-2000; 2000US-0187128P.
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 95; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zynzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 70.8%; Score 17; DB 4; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.7e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CAGGCGCTCAGAUAGGA 24
 |||||:||||:||||:
 DB 17 CAGTGCCTCAGATAGGA 1
 RESULT 8
 ID ADP17626/c
 XX ADP17626 standard; DNA; 25 BP.
 AC ADP17626;
 XX
 DT 26-AUG-2004 (first entry)
 XX Renal cell carcinoma differentially expressed gene probe #4031.
 DE
 XX

KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
 KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
 KW head/neck cancer; differential expression; probe.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048933-A2.
 XX
 PD 10-JUN-2004.
 XX
 XX 21-NOV-2003; 2003WO-US037481.
 XX
 PR 21-NOV-2002; 2002US-0427982P.
 PR 03-APR-2003; 2003US-0459782P.
 XX
 PA (AMHP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BURC/) BURCZYNSKI M E.
 PA (TREP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J A.
 PA (SLOW/) SLOWI D K.
 XX
 XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
 PI Sloni DK;
 XX WPI; 2004-460799/43.
 DR
 XX
 XX Diagnosing non-blood disease such as solid tumor, involves comparing
 PT differential expression profile of specific genes in peripheral blood
 PT sample of subject with reference expression profile of specific genes.
 XX
 XX Disclosure; SEQ ID NO 4362; 350pp; English.
 PS
 XX The invention relate to a method of diagnosing (M1) non-blood disease
 CC such as solid tumor by providing peripheral blood sample of human having
 CC non-blood disease, and comparing an expression profile of specific genes
 CC in the peripheral blood sample to reference expression profile of the
 CC genes, where each of the genes is differentially expressed in peripheral
 CC blood mononuclear cells (PBMCs) of patients having the disease as
 CC compared to PBMCs of normal humans. The method is useful for diagnosing
 CC non-blood disease such as solid tumor. The solid tumor is chosen from
 CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
 CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
 CC sample is a whole blood sample (claimed). (M1) is useful for identifying
 CC genes that are differentially expressed in peripheral blood samples
 CC isolated at different stages of progression, development or treatment of
 CC RCC and/or other solid tumors. This sequence corresponds to a probe to
 CC detect a gene that is differentially expressed and detected by the method
 CC of the invention.
 XX
 SQ Sequence 25 BP; 4 A; 6 C; 4 G; 11 T; 0 U; 0 Other;
 Query Match 70.8%; Score 17; DB 12; Length 25;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CAGUGCCUCAGUAGGA 24
 |||:|||||:|||||
 Db 25 CAGTGCCTCAGATAGGA 9
 RESULT 9
 ABK01532/c
 ID ABK01532 standard; RNA; 17 BP.
 XX
 AC ABK01532;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #802.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyne; zinyne; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 90; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyne (cleaving RNA with an NGN triplet), a zinyne (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states, which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX

SQ Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
Query Match 66.7%; Score 16; DB 4; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.2e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 9 AGUGCCUCAGUAGCA 24
||:||||:||||:
DB 17 AGTGCCCTCAGATAGGA 2
RESULT 10
ID ABK02694/C
XX ABK02694 standard; RNA; 17 BP.
AC ABK02694;
DT 12-MAR-2002 (first entry)
XX Human NOGO Amberyze #366.
DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; TMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO2000159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 139; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA motif) or
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) pr
CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberyze molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 16; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 8.2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAGUGCCUC 16
||:||||:||||:
DB 16 ATTCACCAGGCGCTC 1

RESULT 11

ID ADP48303/C
XX ADP48303 standard; DNA; 22 BP.

AC ADP48303;

DT 09-SEP-2004 (first entry)

DE Human lymphocyte specific tyrosine kinase (Lck) DNA PCR primer #2.

XX Human; lymphocyte specific tyrosine kinase; Lck; PCR; ss;
KW antisense oligonucleotide; phosphorothioate linkage;
KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW hyperproliferative disorder; cancer; cytostatic; primer.

XX Homo sapiens.

OS US2004116365-A1.

FN 17-JUN-2004.

PD 10-DEC-2002; 2002US-00316515.

XX 10-DEC-2002; 2002US-00316515.

PR (ISIS-) ISIS PHARM INC.

XX Borchers AH, Freier SM;

XX WPI; 2004-498280/47.

XX New antisense oligonucleotide compounds, useful for diagnosing,
PT preventing and/or treating diseases or conditions associated with
PT aberrant expression or activity of Lck, such as hyperproliferative
PT disorders.

PS Claim 21; SEQ ID NO 6; 40pp; English.

XX The invention relates to a compound targeted to a nucleic acid molecule
CC encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.

Db 1 CCACGAGTGCCTCAGGT 17

RESULT 14
ABN34093
ID ABN34093 standard; DNA; 60 BP.
XX
AC ABN34093;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6841.
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO20021049-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Paigler S;
XX
XX WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 6841; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 16 A; 10 C; 20 G; 14 T; 0 U; 0 Other;
Query Match 64.2%; Score 15.4; DB 6; Length 60;
Best Local Similarity 76.5%; Pred. NO. 1.9e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 ACCAGGCGCCTCAGGAG 22
|||||:|||||:|
Db 2 ACCAGGCGCCTCAGGAG 18

RESULT 15
AAL27316
ID AAL27316 standard; DNA; 51 BP.
XX
AC AAL27316;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #524.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 1539; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 63.3%; Score 15.2; DB 4; Length 51;
Best Local Similarity 70.0%; Pred. NO. 2.3e+03;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 UCCACCAGGCGCCTCAGGAG 22
:|||||:|||||:|
Db 18 TCCGTCAGTGCCTCAGAC 37

Search completed: July 30, 2005, 15:45:04

Job time : 297.459 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:01:12 ; Search time 2331.57 Seconds
(without alignments)
391.815 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auccaccaguccuagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	66.7	31	1	AI768291
2	14.6	60.8	50	8	AZ452836
3	14	58.3	42	8	AZ452625
C 4	14	58.3	44	8	AZ595168
C 5	14	58.3	57	2	BF143628
C 6	13.8	57.5	58	1	AI327266
C 7	13.6	56.7	33	8	AZ588961
C 8	13.4	55.8	30	8	BH851910
C 9	13.4	55.8	51	9	CL903303
10	13.4	55.8	56	8	BZ660828
C 11	13.2	55.0	31	1	AI443458
C 12	13.2	55.0	41	8	AZ604085
C 13	13.2	55.0	52	1	AA782065
C 14	13.2	55.0	52	9	CL522553
15	13.2	55.0	53	8	CC178725
C 16	13.2	55.0	55	5	BQ565211
C 17	13	54.2	25	8	AZ391620
C 18	13	54.2	28	8	AZ366396
C 19	13	54.2	43	1	AA075907
C 20	13	54.2	46	1	AI463335
21	13	54.2	50	1	AUI02331
22	13	54.2	50	1	AUI02334
23	13	54.2	50	1	AUI02335
24	13	54.2	50	1	AUI02336

25	13	54.2	52	1	AJ742173
26	13	54.2	53	9	CL459396
C 27	13	54.2	58	8	BZ287603
C 28	12.8	53.3	36	1	AV833686
C 29	12.8	53.3	51	8	AZ314162
C 30	12.8	53.3	53	7	CN849116
C 31	12.8	53.3	54	9	AG193022
C 32	12.8	53.3	55	8	BZ767951
C 33	12.6	52.5	48	9	AL940086
C 34	12.6	52.5	50	1	AUI03667
C 35	12.6	52.5	50	2	AUI03674
C 36	12.6	52.5	50	2	AW396348
C 37	12.6	52.5	52	7	NZ9657
C 38	12.6	52.5	54	9	CL528462
C 39	12.6	52.5	55	9	TA108F04P
C 40	12.6	52.5	57	1	AL595919
C 41	12.6	52.5	59	1	AA705635
C 42	12.4	51.7	30	9	TA179H01P
C 43	12.4	51.7	31	8	AZ365377
C 44	12.4	51.7	34	8	AZ309860
C 45	12.4	51.7	37	8	BZ664151

ALIGNMENTS

RESULT 1
AI768291
LOCUS
DEFINITION
AI768291.1 GI:5234800
wgb3f08.x1 Soares NSF P8 9W OT PA P S1 Homo sapiens cDNA clone
IMAGE:2371719 3' similar to TR:060735 060735 GAL7 PROTEIN. ; mRNA
sequence.
ACCESSION
AI768291
VERSION
AI768291.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 31)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1006 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:2371719"
/lab_host="DH10B"
/clone_lib="Soares NSF P8 9W OT PA P S1"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was from
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBSF pool 1:
309384-310919, 323208-325895 Soares NBSF pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NBSF-3W pool 1:
758280-760583, 772104-774407 Soares NBSF pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NbhOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Patina Bonaldo."

ORIGIN

Query Match 66.7%; Score 16; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 9.2e+03;
Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUUCCACGAGCCUCAGAUAGGA 24
|:|||||:|||||:|||||
DB 7 AATCCCAAGTGCCTCATAAGTA 30

RESULT 2

AZ452836 50 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0252H23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0252H23 R, genomic survey sequence.

ACCESSION AZ452836
VERSION 1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: H column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.

FEATURES

Location/Qualifiers

1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0252H23"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

ORIGIN

Query Match 60.8%; Score 14.6; DB 8; Length 50;
Best Local Similarity 71.4%; Pred. No. 4.5e+04;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCACCAGUGCCUCAGAUAGGA 24
|:|||||:|||||:|||||
DB 6 CCACCGTGCCCTCAGCCATGA 26

RESULT 3

AZ452625 42 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0252002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0252002 R, genomic survey sequence.

ACCESSION AZ452625
VERSION 1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: O column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.

FEATURES

Location/Qualifiers

1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0252002"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.3%; Score 14; DB 8; Length 42;
 Best Local Similarity 63.6%; Pred. No. 8.4e+04;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 UUCCACGAGCCUCAGAUAGG 23
 : ||||| : : |||||
 Db 21 TACCACGAGTCACCTAGACAGG 42

RESULT 4
 AZ595168/c
 LOCUS
 DEFINITION 44 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0407C07 R, genomic survey sequence.

ACCESSION AZ595168
 VERSION AZ595168.1 GI:11717358
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weise, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Inert Length: 10000 Std Error: 0.00
 Plate: 0407 row: C column: 07
 Seq primer: CACACAGGAGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES
 source
 1..44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0407C07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.3%; Score 14; DB 8; Length 44;
 Best Local Similarity 59.1%; Pred. No. 8.5e+04;
 Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUUCCACGAGCCUCAGAUAG 22
 : ||||| : : |||||
 Db 35 ATTCAACGAGTGGCTCGCAG 14

RESULT 5
 BF143628/c
 LOCUS
 DEFINITION 57 bp mRNA linear EST 24-OCT-2000
 601790985F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021725 5', mRNA sequence.

ACCESSION BF143628
 VERSION BF143628.1 GI:10982668
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9277 row: i column: 22
 High quality sequence stop: 57.

FEATURES
 source
 1..57
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="IMAGE:4021725"
 /tissue_type="tumor, metastatic to mammary"
 /lab_host="DHI10B"
 /clone_lib="NCI CGAP Lu30"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; transgenic model WNT-1, expression driven by MMV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by life technologies.
 Investigator providing samples: Gilbert Smith, NIH

Query Match 58.3%; Score 14; DB 2; Length 57;
 Best Local Similarity 78.6%; Pred. No. 8.8e+04;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCCACGAGUGCCUC 16
 : ||||| : : |||||
 Db 52 TCCACGAGTGGCTC 39

RESULT 6
 AI327266
 LOCUS
 DEFINITION 58 bp mRNA linear EST 23-DEC-1998
 m05a08.x1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552662 3', similar to SW:IFJX_HUMAN P55884 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT 1, mRNA sequence.

Query Match 58.3%; Score 14; DB 2; Length 57;
 Best Local Similarity 78.6%; Pred. No. 8.8e+04;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCCACGAGUGCCUC 16
 : ||||| : : |||||
 Db 52 TCCACGAGTGGCTC 39

RESULT 6
 AI327266
 LOCUS
 DEFINITION 58 bp mRNA linear EST 23-DEC-1998
 m05a08.x1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552662 3', similar to SW:IFJX_HUMAN P55884 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT 1, mRNA sequence.

```

ACCESSION   AI327266
VERSION      AI327266.1  GI:4061695
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE    1 (bases 1 to 58)
AUTHORS      Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
             Geiseli S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
             Schellberg K., Steptoe M., Tan F., Underwood K., Moore B.,
             Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
             Waterston R.

TITLE        The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
             WashU-HMI Mouse EST Project
             Washington University School of MedicineP
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LML; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:333454
             This clone was previously sequenced on the 5' end only, this new
             data is from the 3' end
             Trace considered overall poor quality
             Possible reversed clone: similarity on wrong strand
             High quality sequence stop: 1.

FEATURES             source
     1..58
         /organism="Mus musculus"
         /mol_type="mRNA"
         /strain="C57BL/6 x CBA"
         /db_xref="taxon:10090"
         /clone="IMAGE:552662"
         /sex="female"
         /tissue_type="lung"
         /dev_stage="6-8 month old"
         /lab_host="SOLR (kanamycin resistant)"
         /clone_lib="Stratagene mouse lung 937302"
         /notes="Organ: lung; Vector: pBluescript SK-; Site 1:
             EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
             Oligo dt. 6-8 month old female lung and 1.5 year old male
             lung were source of mRNA. Average insert size: 1.5 kb;
             Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG
             3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match       57.5%; Score 13.8; DB 1; Length 58;
Best Local Similarity 70.8%; Pred. No. 1.1e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  UCCACCAGUGCCUCAGCA 19
        :|||||:|||||:
Db      6  TCCACCATTGCCTCAGA 22

RESULT 7
AZ588961/c
LOCUS      33 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0397C07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
             clone UUGCLM0397C07 R, genomic survey sequence.
ACCESSION  AZ588961
VERSION     AZ588961.1  GI:11711151
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 33)
REFERENCE   1 (bases 1 to 33)
AUTHORS     Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,

us-09-544-776-5.szl60.rst

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: C column: 07
Seq primer: CACACGAGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.

FEATURES             source
     1..33
         /organism="Mus musculus"
         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGCLM0397C07"
         /sex="Male"
         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGCLM library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."

ORIGIN
Query Match       56.7%; Score 13.6; DB 8; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2  UUCCACCAGUGCCUCAGAU 21
        :|||||:|||||:
Db      22  TTCCCCCATTAGGCTCAGATA 3

RESULT 8
BH851910/c
LOCUS      30 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK 073697.35, 80.x Arabidopsis thaliana TDNA insertion lines
             Arabidopsis thaliana genomic clone SALK_073697.35.80.x, genomic
             survey sequence.
ACCESSION  BH851910
VERSION     BH851910.1  GI:21422781
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

```

REFERENCE
AUTHORS      Alonso,J.M., Leisje,T.J., Barajas,P., Chen,H., Cheuk,R.,
              Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
              Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE        A Sequence-Indexed Library of Insertion Mutations in the
              Arabidopsis Genome
JOURNAL       Unpublished (2001)
COMMENT       Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGnAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel.: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu
              This is single pass sequence recovered from the left border of
              TDNA. This sequence lies within an annotated exon of Atg25180.
              Class: TDNA tagged.

FEATURES
source       Location/Qualifiers
              1..30
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Col-0"
                /db_xref="taxon:3702"
                /clone="SALK_073997.35.80.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                /note=of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          55.8%; Score 13.4; DB 8; Length 30;
Best Local Similarity 56.5%; Pred.No.1.5e+05;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY    1 AUUCCACCAGUGCCUCACGAUAGG 23
      ||||| | :||| |
Db     29 ATTCACACACATTTTCAGATATG 7

RESULT 9
CL903303
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS      Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        1 (bases 1 to 51)
JOURNAL       BayGenomics.ucsf.edu/
COMMENT       Contact: BayGenomics
              Bay Area Functional Genomics Consortium (BayGenomics)
              Email: info@baygenomics.ucsf.edu
              Sequence tag generated by 5' RACE of total RNA from gene trap ES
              cell line. ES cell lines harboring insertion mutation of target
              gene are available upon request from BayGenomics. Annotation
              information available from
              http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACT&TYPE=
              CELL_LINE&BY=RRX310
              Class: Gene Trap.

FEATURES
source       Location/Qualifiers
              1..51
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="129 ola"

```

```

AI443458/c
LOCUS
DEFINITION
  31 bp mRNA linear EST 23-JUL-2004
  Ga33h08.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
  Gm-c1004-1144 5' similar to TR:P93683 P93683 MEMBRANE INTRINSIC
  PROTEIN ; mRNA sequence.
ACCESSION
  AI443458
  AI443458.1 GI:4303310
VERSION
  Glycine max (soybean)
KEYWORDS
  Glycine max
SOURCE
  Glycine max (soybean)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
  Glycine.
REFERENCE
  1 (bases 1 to 31)
  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
  Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
  Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
  Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
  Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
  McCann,R., Waterston,R. and Wilson,R.
  Public Soybean EST Project
  Unpublished (1999)
  Contact: Shoemaker R/Public Soybean EST Project
  Public Soybean EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  When it has been determined, an EST from the other end of this
  clone is listed in the 'Other ESTs on clone' field. Trace
  considered overall poor quality Possible reversed clone: similarity
  on wrong strand This clone is available through: Biogenetic
  Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
  4163; email: info@biogeneticservices.com)
  Seq primer: -40RP from Gibco
  High quality sequence stop: 1
  POLYA=No. Location/Qualifiers
    1..31
      /organism="Glycine max"
      /mol_type="mRNA"
      /cultivar="Williams"
      /db_xref="taxon:3847"
      /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-1144"
      /tissue_type="root"
      /lab_host="XL10-Gold"
      /clone_lib="Gm-c1004"
      /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
      XhoI; Root cDNA. The mRNA was isolated from entire roots
      of 8 day old 'Williams' seedlings which were propagated on
      paper towels with distilled water. Stratagene's cDNA
      Synthesis Kit (catalog #200401) was used to synthesize the
      cDNA. First- strand synthesis was performed with 5-methyl
      dCTP, hence the ligated cDNA is hemimethylated.
      Stratagene's first-strand synthesis primer was used
      [GAGAGAGAGAGAGAGAGACTGCTCGAG(7)-18]. After
      second-strand synthesis, the cDNA ends were 'polished'
      with clone Pfu DNA polymerase, ligated to EcoRI adaptors,
      and phosphorylated. The XhoI site within the first-strand
      synthesis primer was restricted by digestion with XhoI;
      all XhoI sites in the cDNA would be protected by their
      hemimethylated status. The cDNA constructs were
      size-fractionated with a 500bp cutoff, using GibcoBRL Life
      Technologies' cDNA Size Fractionation column. The column
      eluent was then ligated into Stratagene's pBluescript II
      XR Predigested vector (pBluescript II SK(+)) that had been
      digested with EcoRI and XhoI, and phosphorylated). Both
      the white and blue colonies appear to contain recombinant
      plasmids with cDNA inserts. Blue colonies 9n=15) have been
      sequenced, and possess putative cDNA inserts. This library
      was constructed by Dr. Paul Keim & Virginia H. Coryell,

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Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.keim@nau.edu,
virginia.coryell@nau.edu"
ORIGIN
  Query Match 55.0%; Score 13.2; DB 1; Length 31;
  Best Local Similarity 72.2%; Pred. No. 1.9e+05;
  Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
  QY 6 ACCAGUGCCUCACAGUAGG 23
  |||||:|||||:|||||
  28 ACCAGTGGCGGTGATAGG 11
RESULT 12
AZ604085/c
LOCUS
DEFINITION
  41 bp DNA linear GSS 13-DEC-2000
  1M0423G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0423G16 R, genomic survey sequence.
ACCESSION
  AZ604085
  AZ604085.1 GI:11726275
VERSION
  GSS.
KEYWORDS
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
  1 (bases 1 to 41)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausen,A. and Wright,D. Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Place: 0423 row: G column: 16
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 41.
  Location/Qualifiers
    1..41
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0423G16"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated

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with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 13.2; DB 8; Length 41;
Best Local Similarity 61.1%; Pred. No. 2e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AUUCCAGGAGCCUCAG 18
Db 28 ATTCCAGGAGTCATCAG 11

RESULT 13
LOCUS AA782065/c
DEFINITION a147b09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
1360121 3' similar to SW:CD51_HUMAN Q92903 PHOSPHATIDATE
CYTIDYLYLTRANSFERASE 1; mRNA sequence.

ACCESSION AA782065
VERSION AA782065.1 GI:28411396
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 52)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
UNPUBLISHED (1997)

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2110 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
1..52
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1360121"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pTTT3D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-GGTACCAATCTGAAGTGGAGCGCGCCACCAATTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pTT3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

ORIGIN

Query Match 55.0%; Score 13.2; DB 1; Length 52;
Best Local Similarity 61.1%; Pred. No. 2.1e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 UCCACCAGGCGCUCAGU 20
Db 23 TTCCCCGGTGCCTCAGAT 6

RESULT 14
LOCUS CL522553
DEFINITION CL522553
SAM6B01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.

ACCESSION CL522553
VERSION CL522553.1 GI:46149353
KEYWORDS GSS.

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 52)
AUTHORS Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
Ghesquiere, A., Delsevy, M., Glaszmann, J.C. and Guiderdoni, E.

TITLE High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse Genetics
JOURNAL Plant J. (2004) In press
COMMENT Contact: Guiderdoni
UMR PIA Biotrop program
CIRAD

TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
Tel: 33467615629
Fax: 33467615605
Email: emmanuel.guiderdoni@cirad.fr
Class: TDNA tagged.
Location/Qualifiers

FEATURES
source
1..52
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="Planking Sequence Tag of Oryza sativa T-DNA
insertion lines"
/note="PCR was performed on DNA of primary transformants
of Oryza sativa plants. The DNA fragment(s) resulting of
PCR were directly sequenced from the left border to
determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed. Information to order
the corresponding mutant line and a link to a database
providing a graphical display is available from June 2004
at <http://genoplante-info.infobiogen.fr/oryzatagline/>.
This sequence has been generated in the framework of the
French plant genomics program Genoplante
(<http://www.genoplante.org> and
<http://genoplante-info.infobiogen.fr>)."

ORIGIN

Query Match 55.0%; Score 13.2; DB 9; Length 52;
Best Local Similarity 66.7%; Pred. No. 2.1e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 UCCACCAGGCGCUCAGU 20
Db 5 TCCACCACCTGCACAGAT 22

RESULT 15
CC178725

LOCUS CC178725 53 bp mRNA linear GSS 02-MAY-2003
DEFINITION XA060 BayGenomics Gene Trap Library pGT0pfs Mus musculus cDNA, mRNA
sequence.
ACCESSION CC178725
VERSION CC178725.1 GI:30317276
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 53)
REFERENCE BayGenomics.
AUTHORS http://baygenomics.ucsf.edu/
TITLE Unpublished (2001)
JOURNAL Contact: BayGenomics
COMMENT Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XA060
Class: Gene Trap.
Location/Qualifiers
1..53
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0pfs"
/note="Vector: pGT0pfs"

ORIGIN

Query Match 55.0%; Score 13.2; DB 8; Length 53;
Best Local Similarity 61.1%; Pred. No. 2.1e+05;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 UCCACGAGUGCCUCAGAU 20
:|||||:|||||:
Db 13 TCCAGCTGTGCATCAGAT 30

Search completed: July 30, 2005, 18:20:58
Job time : 2336.57 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:05:52 ; Search time 84.3243 Seconds
(without alignments)
465.710 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auuuccaccaguccucagauagga 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	65.0	30	3	US-08-650-726-2
2	15.4	64.2	20	3	US-09-792-594-41
C 3	15.2	63.3	25	4	US-09-396-196G-1657
4	15.2	63.3	25	4	US-09-396-196G-102634
C 5	14.6	60.8	25	4	US-09-396-196G-83857
6	14.6	60.8	32	3	US-09-249-585A-12
7	14.2	59.2	24	1	US-08-488-212A-43
8	14.2	59.2	24	2	US-08-320-306-43
9	14.2	59.2	24	2	US-08-408-209B-43
10	14.2	59.2	24	2	US-08-408-011-43
C 11	14.2	59.2	25	4	US-09-396-196G-81072
C 12	14.2	59.2	25	4	US-09-396-196G-81073
C 13	14.2	59.2	25	4	US-09-396-196G-102633
C 14	14	58.3	25	4	US-09-396-196G-37454
15	14	58.3	25	4	US-09-396-196G-120549
C 16	14	58.3	46	1	US-07-692-995B-45
C 17	13.8	57.5	20	1	US-08-714-626-3
C 18	13.8	57.5	20	2	US-09-705-267A-107
C 19	13.8	57.5	20	4	US-09-705-267A-107
C 20	13.8	57.5	20	5	PCT-US95-0482-3
C 21	13.8	57.5	23	3	US-09-124-238A-30
C 22	13.8	57.5	23	3	US-09-721-975-30
C 23	13.8	57.5	23	4	US-09-986-621-30
C 24	13.8	57.5	25	4	US-09-396-196G-119424
C 25	13.8	57.5	33	3	US-08-169-715-53
C 26	13.6	56.7	25	3	US-08-737-607-37
27	13.6	56.7	25	4	US-09-396-196G-64157

28	13.6	56.7	25	4	US-09-396-196G-124997	Sequence 124997,
29	13.6	56.7	30	1	US-08-045-264A-9	Sequence 9, Appli
30	13.4	55.8	20	4	US-09-705-267A-147	Sequence 147, App
31	13.4	55.8	25	4	US-09-396-196G-50540	Sequence 50540, A
32	13.4	55.8	25	4	US-09-396-196G-62217	Sequence 62217, A
33	13.4	55.8	25	4	US-09-396-196G-70964	Sequence 70964, A
34	13.4	55.8	35	2	US-08-439-819-1	Sequence 1, Appli
35	13.4	55.8	38	4	US-09-764-803B-5	Sequence 5, Appli
C 36	13.4	55.8	47	2	US-08-439-819-2	Sequence 2, Appli
C 37	13.4	55.8	47	4	US-09-422-978-3484	Sequence 3484, Ap
C 38	13.4	55.8	50	3	US-08-959-212-8	Sequence 5, Appli
C 39	13.4	55.8	51	2	US-08-439-819-5	Sequence 8, Appli
C 40	13.4	55.8	60	3	US-08-612-973-95	Sequence 95, Appl
C 41	13.4	55.8	60	3	US-08-927-597-95	Sequence 95, Appl
C 42	13.2	55.0	20	4	US-09-198-452A-6335	Sequence 6335, Ap
C 43	13.2	55.0	25	1	US-08-261-206A-11	Sequence 11, Appl
C 44	13.2	55.0	25	4	US-09-396-196G-84552	Sequence 84552, A
C 45	13.2	55.0	25	4	US-09-396-196G-94333	Sequence 94333, A

ALIGNMENTS

RESULT 1
US-08-650-726-2
; Sequence 2, Application US/08650726
; Patent No. 6027721
; GENERAL INFORMATION:
; APPLICANT: Hamming, Joseph P
; APPLICANT: Aebischer, Patrick
; TITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Ave. of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,726
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Elrif, Ivor R
; REGISTRATION NUMBER: 39,529
; REFERENCE/DOCKET NUMBER: CTI-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 596 9000
; TELEFAX: 212 596 9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-650-726-2

Query Match 65.0%; Score 15.6; DB 3; Length 30;
Best Local Similarity 59.1%; Pred. No. 2.8e+02;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 UUCACCAGUCCUCAGAUAGG 23
:: ||| |:: |||:: |||

```
Db      8 TTTCACTTGTGGCTCAGATAGG 29

RESULT 2
US-09-792-594-41
; Sequence 41, Application US/09792594
; Patent No. 6436706
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL4 EXPRESSION
; FILE REFERENCE: RTS-0209
; CURRENT APPLICATION NUMBER: US/09/792,594
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-792-594-41

Query Match      64.2%; Score 15.4; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 3.2e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCACCAGUGCCUCAGAU 20
Db      1 CCACCAGTGCCTCAGGT 17

RESULT 3
US-09-396-196G-1657/c
; Sequence 1657, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1657

Query Match      63.3%; Score 15.2; DB 4; Length 25;
Best Local Similarity 70.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGUGCCUCAGAU 20
Db      22 ATGCCACGAGTGCACACAGAT 3

RESULT 4
US-09-396-196G-102634
; Sequence 102634, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: METHODS FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

Db      4 CCACCAGUGCCUCAGAUAGA 24
Db      22 CCACCTAGTGGCTCTGTTAGGA 2

RESULT 6
US-09-249-585A-12
; Sequence 12, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83857
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83857

Query Match      60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      4 CCACCAGUGCCUCAGAUAGA 24
Db      22 CCACCTAGTGGCTCTGTTAGGA 2

RESULT 5
US-09-396-196G-83857/c
; Sequence 83857, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83857
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83857

Query Match      63.3%; Score 15.2; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AUUCCACCAGUGCCUCAGAU 20
Db      1 ATTCAACCACTGACTAAGAT 20

Query Match      63.3%; Score 15.2; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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; LOCATION: (1)...(32)
; OTHER INFORMATION: oligonucleotide used for RT-PCR amplification of Bcl2
US-09-349-585A-12

Query Match          60.8%; Score 14..6; DB 3; Length 32;
Best Local Similarity 61.9%; Pred. No. 8.7e+02;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 UCCACCAGUGCCUCAGAUAGG 23
   :|||:|:|:|:|:|:|
Db 12 TTCACCTGTGGCTCAGATAGG 32

RESULT 7
US-08-488-212A-43
; Sequence 43, Application US/08488212A
; Patent No. 5665355
; GENERAL INFORMATION:
; APPLICANT: Primi, Daniele
; TITLE OF INVENTION: Diagnosis and Treatment of
; TITLE OF INVENTION: AIDS Onset
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas
; ADDRESSEE: Popovich & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea
; COMPUTER: 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,212A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,485
; FILING DATE: No. 5665355ember 9, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; REFERENCE/DOCKET NUMBER: 3678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
; MOLECULE TYPE: Va region)
; HYPOTHETICAL: No
; ORIGINAL SOURCE: Synthesized using
; ORIGINAL SOURCE: oligonucleotide synthesis machine
; PUBLICATION INFORMATION:
; AUTHORS: Imberti, Luisa; Sottini, Alessandra; Puoti, Massimo; Primi,
; AUTHORS: Alessandra; Bettinardi, Daniele
; TITLES: Selective depletion in HIV Infection
; TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
; JOURNAL: Science
; VOLUME: 254
; ISSUE: 5033
; PAGES: 860-862

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US-08-320-306-43

Query Match 59.2%; Score 14.2; DB 2; Length 24;
Best Local Similarity 68.4%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCCACGAGCCUCACAGA 19
|::| ||| |||: |||
Db 5 ATTCAACAGCGCCTCAGA 23

RESULT 9

US-08-488-209B-43
; Sequence 43, Application US/08488209B
; Patent No. 5925513
; GENERAL INFORMATION:
; APPLICANT: Primi, Daniele
; TITLE OF INVENTION: Diagnosis and Treatment of
; TITLE OF INVENTION: AIDS Onset
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas
; ADDRESSEE: Popovich & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea
; COMPUTER: 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,209B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,485
; FILING DATE: No. 5925513ember 9, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; REFERENCE/DOCKET NUMBER: 3678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
; MOLECULE TYPE: (Va region)
; HYPOTHETICAL: No
; ORIGINAL SOURCE: Synthesized using
; ORIGINAL SOURCE: oligonucleotide synthesis machine
; PUBLICATION INFORMATION:
; AUTHORS: Imberti, Luisa; Sottini,
; AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
; AUTHORS: Daniele
; TITLE: Selective Depletion in HIV Infection
; TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
; JOURNAL: Science
; VOLUME: 254
; ISSUE: 5033
; PAGES: 860-862
; PUBLICATION DATE: No. 5925513ember 8, 1991
US-08-488-209B-43

Query Match 59.2%; Score 14.2; DB 2; Length 24;
Best Local Similarity 68.4%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCCACGAGCCUCACAGA 19
|::| ||| |||: |||
Db 5 ATTCAACAGCGCCTCAGA 23

RESULT 10

US-08-408-011-43
; Sequence 43, Application US/08408011
; Patent No. 5928642
; GENERAL INFORMATION:
; APPLICANT: Primi, Daniele
; TITLE OF INVENTION: Diagnosis and Treatment of
; TITLE OF INVENTION: AIDS Onset
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas E. Popovich, Thomas
; ADDRESSEE: Popovich & Associates
; STREET: 80 South 8th Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-2111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible Compaq Prolinea
; COMPUTER: 4/66
; OPERATING SYSTEM: MS-DOS Version 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,011
; FILING DATE: 18-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,485
; FILING DATE: No. 5928642ember 9, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. Popovich
; REGISTRATION NUMBER: 30099
; REFERENCE/DOCKET NUMBER: 3678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 334-8991
; TELEFAX: (612) 334-8994
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
; MOLECULE TYPE: (Va region)
; HYPOTHETICAL: No
; ORIGINAL SOURCE: Synthesized using
; ORIGINAL SOURCE: oligonucleotide synthesis machine
; PUBLICATION INFORMATION:
; AUTHORS: Imberti, Luisa; Sottini,
; AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
; AUTHORS: Daniele
; TITLE: Selective Depletion in HIV Infection
; TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
; JOURNAL: Science
; VOLUME: 254
; ISSUE: 5033
; PAGES: 860-862
; PUBLICATION DATE: No. 5928642ember 8, 1991
US-08-408-011-43

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Query Match          59.2%; Score 14.2; DB 2; Length 24;
Best Local Similarity 68.4%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCACACGAGCCUCACAGA 19
    ||||| ||||| ||||| |||||
Db 5 ATTCACACGAGCCCTCAGA 23

RESULT 11
US-09-396-196G-81072/c
; Sequence 81072, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81072
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81072

Query Match          59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 CACGAGCCUCAGAUAGG 23
    ||||| ||||| ||||| |||||
Db 25 CACGAGTTCCACAGATGG 7

RESULT 12
US-09-396-196G-81073/c
; Sequence 81073, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81073

Query Match          59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 CACGAGCCUCAGAUAGG 23
    ||||| ||||| ||||| |||||
Db 19 CACGAGTTCCACAGATGG 1

RESULT 13
US-09-396-196G-102633
; Sequence 102633, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102633

Query Match          59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 63.2%; Pred. No. 1.3e+03;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AUUCACACGAGCCUCACAGA 19
    ||||| ||||| ||||| |||||
Db 7 ATTCACACGAGTACTAGAGA 25

RESULT 14
US-09-396-196G-37454/c
; Sequence 37454, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-37454

Query Match          58.3%; Score 14; DB 4; Length 25;
Best Local Similarity 63.6%; Pred. No. 1.6e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 UCCACGAGCCUCAGAUAGGA 24
    ||||| ||||| ||||| |||||
Db 23 TCCAGCTGTGTCTCCGAAGGA 2

RESULT 15
US-09-396-196G-120549
; Sequence 120549, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
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; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-120549

Query Match 58.1%; Score 14; DB 4; Length 25;
Best Local Similarity 59.1%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 UUCACCCAGUGCCUCAGAUAGG 23
::| |||||: ||| |||
Db 1 TTCATCCAGTGGCTGAGAGAGG 22

Search completed: July 30, 2005, 18:25:13
Job time : 85.3243 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:29:53 ; Search time 451.784 Seconds
(without alignments)
343.829 Million cell updates/sec

Title: US-09-544-776-5

Perfect score: 24

Sequence: 1 auccaccagcucacgaugga 24

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 8371272

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	91.7	25	19	US-10-717-597-4363
C 2	21	87.5	25	21	US-10-956-157-183480
C 3	21	87.5	25	21	US-10-956-157-183481
C 4	21	87.5	25	21	US-10-956-157-183482
C 5	21	87.5	25	21	US-10-956-157-183483
C 6	21	87.5	25	21	US-10-956-157-183484
C 7	17	70.8	17	10	US-09-780-533A-1533

Query Match 91.7%; Score 22; DB 19; Length 25;
Best Local Similarity 77.3%; Pred. No. 0.94;

C 8	17	70.8	17	10	US-09-780-533A-1534	Sequence 1534, Ap
C 9	17	70.8	17	10	US-09-780-533A-1774	Sequence 1774, Ap
C 10	17	70.8	17	10	US-09-780-533A-2081	Sequence 2081, Ap
C 11	17	70.8	17	10	US-09-780-533A-2693	Sequence 2693, Ap
C 12	17	70.8	25	19	US-10-717-597-4362	Sequence 4362, Ap
C 13	16.2	67.5	25	21	US-10-719-900-292913	Sequence 292913, Ap
C 14	16	66.7	17	10	US-09-780-533A-1532	Sequence 1532, Ap
C 15	16	66.7	17	10	US-09-780-533A-2694	Sequence 2694, Ap
C 16	15.8	65.8	25	21	US-10-719-900-448746	Sequence 448746, Ap
C 17	15.8	65.8	25	21	US-10-719-900-832455	Sequence 832455, Ap
C 18	15.8	65.8	25	21	US-10-719-956-457031	Sequence 457031, Ap
C 19	15.6	65.0	22	19	US-10-316-515-6	Sequence 6, Appli
C 20	15.6	65.0	25	21	US-10-719-900-885669	Sequence 885669, Ap
C 21	15.6	65.0	25	22	US-10-719-956-252140	Sequence 252140, Ap
C 22	15.4	64.2	60	10	US-09-908-975-6841	Sequence 6841, Ap
C 23	15.2	63.3	25	21	US-10-809-189-1657	Sequence 1657, Ap
C 24	15.2	63.3	25	21	US-10-809-189-102634	Sequence 102634, Ap
C 25	15.2	63.3	25	22	US-10-719-956-270018	Sequence 270018, Ap
C 26	15	62.5	17	10	US-09-780-533A-714	Sequence 714, App
C 27	15	62.5	17	10	US-09-780-533A-2082	Sequence 2082, Ap
C 28	15	62.5	25	21	US-10-719-900-747466	Sequence 747466, Ap
C 29	15	62.5	25	22	US-10-719-956-66724	Sequence 66724, A
C 30	15	62.5	25	22	US-10-719-956-71795	Sequence 71795, A
C 31	15	62.5	25	22	US-10-719-956-539128	Sequence 539128, Ap
C 32	15	62.5	50	17	US-10-131-827-660	Sequence 660, App
C 33	14.8	61.7	25	21	US-10-719-900-864194	Sequence 864194, A
C 34	14.8	61.7	25	22	US-10-719-956-88068	Sequence 88068, A
C 35	14.8	61.7	25	22	US-10-719-956-516451	Sequence 516451, A
C 36	14.6	60.8	25	15	US-10-098-2638-32948	Sequence 32948, A
C 37	14.6	60.8	25	21	US-10-719-900-244717	Sequence 244717, Ap
C 38	14.6	60.8	25	21	US-10-719-900-292914	Sequence 292914, Ap
C 39	14.6	60.8	25	21	US-10-719-900-370596	Sequence 370596, Ap
C 40	14.6	60.8	25	21	US-10-719-900-792127	Sequence 792127, Ap
C 41	14.6	60.8	25	21	US-10-719-900-868576	Sequence 868576, Ap
C 42	14.6	60.8	25	21	US-10-809-189-83857	Sequence 83857, A
C 43	14.6	60.8	25	21	US-10-956-157-300308	Sequence 300308, A
C 44	14.6	60.8	25	22	US-10-719-956-25044	Sequence 25044, A
C 45	14.6	60.8	25	22	US-10-719-956-249546	Sequence 249546, Ap

ALIGNMENTS

RESULT 1

US-10-717-597-4363/c
; Sequence 4363, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10717597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-4363

QY 2 UUCACCAAGCCUACAGUAG 22
 DB 25 TTCCACCAAGTGCCTCAGATAG 5

RESULT 7

US-09-780-533A-1533/c
 ; Sequence 1533, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1533
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-1533

Query Match 70.8%; Score 17; DB 10; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.5e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCCACCAAGCCUACAGA 19
 DB 17 TCCACCAAGTGCCTCAGA 1

RESULT 8

US-09-780-533A-1534/c
 ; Sequence 1534, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1534
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-1534

Query Match 70.8%; Score 17; DB 10; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.5e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUUCCACCAAGCCUACA 17
 DB 17 ATTCCACCAAGTGCCTCA 1

RESULT 9

US-09-780-533A-1774/c
 ; Sequence 1774, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1774
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-1774

Query Match 70.8%; Score 17; DB 10; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.5e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGUGCCUACAGUAGGA 24
 DB 17 CAGTGCCTCAGATAGGA 1

RESULT 10

US-09-780-533A-2081/c
 ; Sequence 2081, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2081
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-2081

Query Match 70.8%; Score 17; DB 10; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.5e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 CACCAGUGCCUACAGUA 21
 DB 17 CACCAGTGCCTCAGATA 1

RESULT 11

US-09-780-533A-2693/c
 ; Sequence 2693, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim

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; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2693
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2693

Query Match      70.8%; Score 17; DB 10; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACCAGGCCUCAGAUAG 22
DB      17 ACCAGTGCCTCAGATAG 1

RESULT 12
US-10-717-597-4362/c
; Sequence 4362, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-4362

Query Match      70.8%; Score 17; DB 19; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.6e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGUGCCUCAGAUAGGA 24
DB      25 CAGTGCCTCAGATAGGA 9

RESULT 13
US-10-719-900-292913/c
; Sequence 292913, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-292913

Query Match      67.5%; Score 16.2; DB 21; Length 25;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 UCCACGAGUGCCUCACAGUAGG 23
DB      25 TCATCAGTGCCTCACACAGG 5

RESULT 14
US-09-780-533A-1532/c
; Sequence 1532, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1532
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1532

Query Match      66.7%; Score 16; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 7.8e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      9 AGUGCCUCAGAUAGGA 24
DB      17 AGTGCCTCAGATAGGA 2

RESULT 15
US-09-780-533A-2694/c
; Sequence 2694, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2694
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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US-09-780-533A-2694

Query Match 66.7%; Score 16; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.8e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCCACGAGGCTC 16
|:|||||:|:|:|
Db 16 AATCCACGAGGCTC 1

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Job time : 452.784 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 15:29:53 ; Search time 470.608 Seconds
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343.829 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacuucaggaucagauagccc 25

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Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16.6	66.4	25	21	US-10-719-900-329433
3	16.2	64.8	60	10	US-09-908-975-14572
4	16	64.0	17	10	US-09-780-533A-568
5	16	64.0	25	21	US-10-956-157-21957
6	16	64.0	25	21	US-10-956-157-21960
7	16	64.0	25	21	US-10-956-157-97484

C 8	16	64.0	25	21	US-10-956-157-135597
C 9	16	64.0	41	18	US-10-453-827-239
C 10	16	64.0	60	19	US-10-642-093-46
C 11	16	64.0	60	19	US-10-795-002-46
C 12	15.6	62.4	25	21	US-10-719-900-41315
C 13	15.6	62.4	25	21	US-10-956-157-21946
C 14	15.6	62.4	25	21	US-10-956-157-21947
C 15	15.6	62.4	25	21	US-10-956-157-21963
C 16	15.6	62.4	25	21	US-10-956-157-97462
C 17	15.6	62.4	25	21	US-10-956-157-97463
C 18	15.6	62.4	25	21	US-10-956-157-179966
C 19	15.6	62.4	25	22	US-10-719-956-618759
C 20	15.4	61.6	25	21	US-10-719-900-895386
C 21	15.4	61.6	25	22	US-10-719-956-269689
C 22	15.4	61.6	25	22	US-10-719-956-441174
C 23	15.2	60.8	25	22	US-10-719-956-578410
C 24	15	60.0	17	10	US-09-780-533A-567
C 25	15	60.0	17	10	US-09-780-533A-1442
C 26	15	60.0	25	21	US-10-719-900-168271
C 27	15	60.0	25	21	US-10-719-900-541175
C 28	15	60.0	25	21	US-10-719-900-876063
C 29	15	60.0	25	21	US-10-809-189-88973
C 30	15	60.0	25	22	US-10-719-956-72988
C 31	15	60.0	60	10	US-09-908-975-6447
C 32	14.8	59.2	23	19	US-10-627-253A-30
C 33	14.6	58.4	21	20	US-10-751-736-25240
C 34	14.6	58.4	21	20	US-10-751-736-25351
C 35	14.6	58.4	25	21	US-10-719-900-292748
C 36	14.6	58.4	25	21	US-10-719-900-613272
C 37	14.6	58.4	25	21	US-10-719-900-614140
C 38	14.6	58.4	25	21	US-10-719-900-630466
C 39	14.6	58.4	25	21	US-10-719-900-630467
C 40	14.6	58.4	25	21	US-10-956-157-21945
C 41	14.6	58.4	25	21	US-10-956-157-97461
C 42	14.6	58.4	25	22	US-10-719-956-38250
C 43	14.6	58.4	25	22	US-10-719-956-64979
C 44	14.6	58.4	25	22	US-10-719-956-347262
C 45	14.6	58.4	25	22	US-10-719-956-347263

ALIGNMENTS

RESULT 1
US-10-719-900-329432
; Sequence 329432, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329432
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-329432

Query Match 66.4%; Score 16.6; DB 21; Length 25;
Best Local Similarity 60.9%; Pred. No. 6.4e+02;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGAUUCCAGAUUCC 23

Db 1 CATCTCCGATCCTAGATATGC 23

RESULT 2

US-10-719-900-329433
; Sequence 329433, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329433
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-329433

Query Match 66.4%; Score 16.6; DB 21; Length 25;
Best Local Similarity 60.9%; Pred. No. 6.4e+02;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 23
|||:|||||:|||||:
Db 1 CATCTCCGGATGCTAGATATGC 23

RESULT 3
US-09-908-975-14572/c
; Sequence 14572, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14572
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14572

Query Match 64.8%; Score 16.2; DB 10; Length 60;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 5 UUCAGGAUUCAGGAUAGCC 25
|||:|||||:|||||:
Db 23 TTCACGGTCCAGATATGCC 3

RESULT 4
US-09-780-533A-568/c
; Sequence 568, Application US/09780533A
; Publication No. US2003006011A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat

; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 568
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-568

Query Match 64.0%; Score 16; DB 10; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAUUCACAGAUAGCCC 25
|||:|||||:|||||:
Db 16 GATTCAGATATGCC 1

RESULT 5
US-10-956-157-21957/c
; Sequence 21957, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21957

Query Match 64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAACUUCAGGAUCCAGAUAGCC 24
|||:|||||:|||||:
Db 24 CCATCCAGGATGTCAGATATGAC 1

RESULT 6
US-10-956-157-21960/c
; Sequence 21960, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21960
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21960

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Query Match 64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCC 24
   |||:||||:||||:||||:|
Db 25 CCACTCCAGGATGTCAGATATGAC 2

RESULT 7
US-10-956-157-97484/c
; Sequence 97484, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97484

Query Match 64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUCCAGAUAGCC 24
   |||:||||:||||:||||:|
Db 24 CCACTCCAGGATGTCAGATATGAC 1

RESULT 8
US-10-956-157-135597/c
; Sequence 135597, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 135597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-135597

Query Match 64.0%; Score 16; DB 21; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAUUCAGAUAGCC 25
   |||:||||:||||:||||:|
Db 17 GATTCCAGATATGCC 2

RESULT 9
US-10-453-827-239/c
; Sequence 239, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
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; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-453-827-239

Query Match 64.0%; Score 16; DB 18; Length 41;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCC 25
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Db 34 AACTACAGGATTACATCTGTCC 11

RESULT 10
US-10-642-093-46
; Sequence 46, Application US/10642093
; Publication No. US20040106555A1
; GENERAL INFORMATION:
; APPLICANT: German, Michael S.
; APPLICANT: Lin, Joseph
; TITLE OF INVENTION: NEUROGENIN3 AND PRODUCTION OF PANCREATIC
; TITLE OF INVENTION: ISLET CELLS
; FILE REFERENCE: UCSF-129CIP2
; CURRENT APPLICATION NUMBER: US/10/642,093
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/US02/11165
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 09/817,360
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/535,145
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/128,180
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-642-093-46

Query Match 64.0%; Score 16; DB 19; Length 60;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCC 25
   |||:||||:||||:||||:|
Db 2 ATCTTCGGGAATCCAGCTGTGCC 25

RESULT 11
US-10-795-002-46
; Sequence 46, Application US/10795002
; Publication No. US20040152168A1
; GENERAL INFORMATION:
; APPLICANT: German, Michael S.
; APPLICANT: Lin, Joseph
; TITLE OF INVENTION: NEUROGENIN3 AND PRODUCTION OF PANCREATIC
; TITLE OF INVENTION: ISLET CELLS
; FILE REFERENCE: UCSF-129CIP2
; CURRENT APPLICATION NUMBER: US/10/795,002
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Job time : 471.608 secs

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Run on: July 30, 2005, 15:29:53 ; Search time 470.608 Seconds
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Title: US-09-544-776-3

Perfect score: 25

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Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	96.0	25	21	US-10-719-900-63085, A
C 3	24	96.0	25	21	US-10-956-157-164478, A
C 4	24	96.0	25	21	US-10-956-157-164479, A
C 5	24	96.0	25	21	US-10-956-157-164480, A
C 6	24	96.0	25	21	US-10-956-157-164481, A
C 7	24	96.0	25	21	US-10-956-157-164482, A

C 8	22.4	89.6	25	21	US-10-719-900-63086	Sequence 63086, A
C 9	19.8	79.2	25	22	US-10-719-956-169644	Sequence 169644, A
C 10	18.2	72.8	25	22	US-10-719-956-169643	Sequence 169643, A
C 11	17.2	68.8	25	21	US-10-956-157-158471	Sequence 158471, A
C 12	17	68.0	17	10	US-09-780-533A-561	Sequence 561, App
C 13	17	68.0	17	10	US-09-780-533A-1429	Sequence 1429, App
C 14	17	68.0	17	10	US-09-780-533A-1430	Sequence 1430, App
C 15	17	68.0	17	10	US-09-780-533A-1737	Sequence 1737, App
C 16	17	68.0	17	10	US-09-780-533A-2029	Sequence 2029, App
C 17	17	68.0	17	10	US-09-780-533A-2284	Sequence 2284, App
C 18	16.6	66.4	25	22	US-10-719-956-146225	Sequence 146225, A
C 19	16.4	65.6	25	22	US-10-384-339C-172	Sequence 172, App
C 20	16.4	65.6	24	19	US-10-384-339C-173	Sequence 173, App
C 21	16	64.0	17	10	US-09-780-533A-2028	Sequence 2028, App
C 22	16	64.0	25	21	US-10-956-157-238770	Sequence 238770, A
C 23	15.8	63.2	60	10	US-09-908-975-5561	Sequence 5561, App
C 24	15.6	62.4	25	21	US-10-719-900-195537	Sequence 195537, A
C 25	15.6	62.4	25	22	US-10-719-956-123417	Sequence 123417, A
C 26	15.4	61.6	17	10	US-09-848-754A-934	Sequence 934, App
C 27	15.4	61.6	17	10	US-09-848-754A-934	Sequence 934, App
C 28	15.4	61.6	20	17	US-10-380-931-38	Sequence 38, Appl
C 29	15.2	60.8	25	21	US-10-719-900-115543	Sequence 115543, A
C 30	15.2	60.8	25	21	US-10-719-900-392915	Sequence 392915, A
C 31	15.2	60.8	25	22	US-10-719-956-521423	Sequence 521423, A
C 32	15	60.0	17	10	US-09-780-533A-1431	Sequence 1431, App
C 33	15	60.0	25	21	US-10-719-900-602483	Sequence 602483, A
C 34	15	60.0	25	22	US-10-719-956-146226	Sequence 146226, A
C 35	15	60.0	25	22	US-10-719-956-377866	Sequence 377866, A
C 36	15	60.0	25	22	US-10-719-956-575601	Sequence 575601, A
C 37	15	60.0	60	10	US-09-908-975-7591	Sequence 7591, App
C 38	15	60.0	60	10	US-09-908-975-20410	Sequence 20410, A
C 39	15	60.0	60	21	US-10-764-420-3553	Sequence 3553, App
C 40	15	60.0	60	21	US-10-764-420-3604	Sequence 3604, App
C 41	14.8	59.2	25	21	US-10-719-900-619461	Sequence 619461, A
C 42	14.8	59.2	25	22	US-10-719-956-302908	Sequence 302908, A
C 43	14.8	59.2	25	22	US-10-719-956-412824	Sequence 412824, A
C 44	14.6	58.4	25	21	US-10-719-900-73849	Sequence 73849, A
C 45	14.6	58.4	25	21	US-10-719-900-851430	Sequence 851430, A

ALIGNMENTS

RESULT 1
US-10-956-157-169389/c
; Sequence 169389, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-169389

Query Match	100.0%	Score 25;	DB 21;	Length 25;
Best Local Similarity	72.0%	Pred. No. 0.034;		
Matches	18;	Conservative	7;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	CUGGAAGCUGGAGCAACACCCUUG	25	
Db	25	CTGGATAGCTTGGATCACACCCCTTG	1	

RESULT 2


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; Sequence 164482, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164482
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-164482

Query Match          96.0%; Score 24; DB 21; Length 25;
Best Local Similarity 70.8%; Pred. No. 0.1;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUU 24
Db 24 CTGGATAGCTTGGATCACCCTT 1

RESULT 8
US-10-719-900-63086/c
; Sequence 63086, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 63086
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-63086

Query Match          89.6%; Score 22.4; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.63;
Matches 16; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUCACACCCUU 24
Db 24 CTGGATAGCTTGGATCACCCTT 1

RESULT 9
US-10-719-956-169644/c
; Sequence 169644, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169644
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Rattus norvegicus
US-10-719-956-169644

Query Match          79.2%; Score 19.8; DB 22; Length 25;
Best Local Similarity 65.2%; Pred. No. 12;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
Db 25 TGGATAGCTTGGATCACCCTT 3

RESULT 10
US-10-719-956-169643/c
; Sequence 169643, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-169643

Query Match          72.8%; Score 18.2; DB 22; Length 25;
Best Local Similarity 60.9%; Pred. No. 69;
Matches 14; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 UGGAUAGCUUGGAUCACACCCUU 24
Db 25 TGGATAGCTTGGATCACCCTT 3

RESULT 11
US-10-956-157-158471/c
; Sequence 158471, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-158471

Query Match          68.8%; Score 17.2; DB 21; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.1e+02;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAUAGCUUGGAUCACACCCUU 24
Db 22 GGACAGCTTGGATCACCCTT 1

RESULT 12
US-09-780-533A-561/c
; Sequence 561, Application US/09780533A
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; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 561
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-561

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      5 AUAGCUUGGAUCACACC 21
Db      17 ATAGCTTGGATCACAC 1

RESULT 13
US-09-780-533A-1429/c
; Sequence 1429, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1429
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1429

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAUAGCUUGGAUCACAC 20
Db      17 GATAGCTTGGATCACAC 1

RESULT 14
US-09-780-533A-1430/c
; Sequence 1430, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1430
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1430

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 GCUUGGAUCACACCCU 24
Db      17 GCTTGGATCACACCC 1

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; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1430
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1430

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGAUAGCUUGGAUCACA 19
Db      17 GGATAGCTTGGATCACAC 1

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; Sequence 1737, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1737
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1737

Query Match      68.0%; Score 17; DB 10; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      8 GCUUGGAUCACACCCU 24
Db      17 GCTTGGATCACACCC 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	24	100.0	170	18	US-10-085-783A-57815
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C 8	24	100.0	370	18	US-10-085-783A-54131	Sequence 54131, A
C 9	24	100.0	468	17	US-10-242-535A-31372	Sequence 31372, A
C 10	24	100.0	468	18	US-10-085-783A-31372	Sequence 31372, A
C 11	24	100.0	972	17	US-10-437-931-1	Sequence 1, Appli
C 12	24	100.0	1610	9	US-09-765-205-5	Sequence 5, Appli
C 13	24	100.0	1610	21	US-10-347-669-5	Sequence 52, Appli
C 14	24	100.0	1785	17	US-10-439-388-62	Sequence 62, Appli
C 15	24	100.0	1785	21	US-10-956-157-1705	Sequence 1705, Ap
C 16	24	100.0	2235	14	US-10-060-036-54	Sequence 54, Appli
C 17	24	100.0	4053	9	US-09-758-140-5	Sequence 5, Appli
C 18	24	100.0	4053	9	US-09-972-599A-5	Sequence 5, Appli
C 19	24	100.0	4053	19	US-10-717-597-310	Sequence 310, App
C 20	24	100.0	4632	14	US-10-060-036-53	Sequence 53, Appli
C 21	24	100.0	4710	10	US-09-764-891-7385	Sequence 7385, Ap
C 22	22	91.7	25	19	US-10-717-597-4363	Sequence 4363, Ap
C 23	22	91.7	211	14	US-10-004-427-51	Sequence 51, Appli
C 24	22	91.7	211	21	US-10-984-752-51	Sequence 51, Appli
C 25	22	91.7	360	9	US-09-764-846-60	Sequence 60, Appli
C 26	22	91.7	360	14	US-10-091-483-60	Sequence 60, Appli
C 27	22	91.7	377	9	US-09-764-846-132	Sequence 132, App
C 28	22	91.7	377	14	US-10-091-483-132	Sequence 132, App
C 29	22	91.7	410	10	US-09-918-995-22263	Sequence 22263, A
C 30	22	91.7	602	20	US-10-357-930-49749	Sequence 49749, A
C 31	22	91.7	633	20	US-10-357-930-19960	Sequence 19960, A
C 32	22	91.7	994	11	US-09-978-360A-110	Sequence 110, App
C 33	22	91.7	1160	14	US-10-175-523-156	Sequence 156, App
C 34	22	91.7	1400	21	US-10-956-157-9762	Sequence 9762, Ap
C 35	22	91.7	1400	21	US-10-956-157-9763	Sequence 9763, Ap
C 36	22	91.7	1400	21	US-10-956-157-9765	Sequence 9765, Ap
C 37	22	91.7	1400	21	US-10-956-157-9766	Sequence 9766, Ap
C 38	22	91.7	1400	21	US-10-956-157-9767	Sequence 9767, Ap
C 39	22	91.7	1514	9	US-09-823-245A-349	Sequence 349, App
C 40	22	91.7	1609	21	US-10-956-157-4527	Sequence 4527, Ap
C 41	22	91.7	1798	19	US-10-466-258-10	Sequence 10, Appli
C 42	22	91.7	1798	22	US-10-466-391A-10	Sequence 10, Appli
C 43	22	91.7	1980	17	US-10-220-891-22	Sequence 22, Appli
C 44	22	91.7	2050	21	US-10-956-157-4530	Sequence 4530, Ap
C 45	22	91.7	2052	19	US-10-466-258-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-242-535A-33274/c
; Sequence 33274, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33274
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-33274

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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;


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; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54131
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-54131

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Best Local Similarity 79.2%; Pred. No. 0.11;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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US-10-242-535A-31372/c
; Sequence 31372, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31372
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-31372

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Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 409 ATTCCACCAGTGCTCAGATAGGA 386
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US-10-085-783A-31372/c
; Sequence 31372, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.

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; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
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; SEQ ID NO 31372
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-31372

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Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 409 ATCCACCAGTGCCTCAGATAGGA 386

RESULT 11
US-10-437-931-1/c
; Sequence 1, Application US/10437931
; Publication No. US20030215868A1
; GENERAL INFORMATION:
; APPLICANT: Seeman, Philip
; APPLICANT: No. US20030215868A1a1, Gabriela
; APPLICANT: Tallierico, Teresa
; TITLE OF INVENTION: Method of Detecting Schizophrenia
; FILE REFERENCE: 13459-1
; CURRENT APPLICATION NUMBER: US/10/437,931
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: UK 0211212.6
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-437-931-1

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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 265 ATCCACCAGTGCCTCAGATAGGA 242

RESULT 12
US-09-765-205-5/c
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0

; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
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; ORGANISM: Human
; US-10-085-783A-31372

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Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 409 ATCCACCAGTGCCTCAGATAGGA 386

RESULT 11
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; Sequence 1, Application US/10437931
; Publication No. US20030215868A1
; GENERAL INFORMATION:
; APPLICANT: Seeman, Philip
; APPLICANT: No. US20030215868A1a1, Gabriela
; APPLICANT: Tallierico, Teresa
; TITLE OF INVENTION: Method of Detecting Schizophrenia
; FILE REFERENCE: 13459-1
; CURRENT APPLICATION NUMBER: US/10/437,931
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: UK 0211212.6
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-437-931-1

Query Match 100.0%; Score 24; DB 17; Length 972;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 265 ATCCACCAGTGCCTCAGATAGGA 242

RESULT 12
US-09-765-205-5/c
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
; US-09-765-205-5

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Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1518 ATCCACCAGTGCCTCAGATAGGA 1495

RESULT 13
US-10-347-669-5/c
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
; US-10-347-669-5

Query Match 100.0%; Score 24; DB 21; Length 1610;
Best Local Similarity 79.2%; Pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1518 ATCCACCAGTGCCTCAGATAGGA 1495

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; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-439-388-62

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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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US-10-956-157-1705/c
; Sequence 1705, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1705
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-1705

Query Match 100.0%; Score 24; DB 21; Length 1785;
Best Local Similarity 79.2%; pred. No. 0.12;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1078 ATCCACCAGTGCTCAGATAGGA 1055

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 12:02:47 ; Search time 483.108 Seconds
(without alignments)
334.933 Million cell updates/sec

Title: US-09-544-776-4

Perfect score: 25

Sequence: 1 caacucaggauccagauagccc 25

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Searched: 7287783 seqs, 3236178273 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	19.2	76.8	597	20	US-10-425-115-117468
C 3	19.2	76.8	40304	11	US-09-997-722-280
C 4	19.2	76.8	86574	19	US-10-775-169-173
5	18.6	74.4	391	9	US-09-960-352-8669
6	18.6	74.4	402	9	US-09-960-352-11019
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C 8	18.6	74.4	1830121	17	US-10-329-670-1	Sequence 1, Appli
C 9	18.6	74.4	1830121	20	US-10-158-865-1	Sequence 1, Appli
C 10	18.6	74.4	1830121	22	US-10-981-687-1	Sequence 1, Appli
C 11	18.4	73.6	564	22	US-10-972-079-58889	Sequence 58889, A
C 12	18.4	73.6	8473	9	US-09-851-682A-2	Sequence 2, Appli
C 13	18	72.0	601	22	US-10-893-315-332	Sequence 332, App
C 14	18	72.0	601	22	US-10-893-315-1543	Sequence 1543, Ap
C 15	18	72.0	117231	22	US-10-893-315-129	Sequence 129, App
C 16	18	72.0	119226	22	US-10-893-315-159	Sequence 159, App
C 17	18	72.0	119313	22	US-10-893-315-164	Sequence 164, App
C 18	18	72.0	149382	21	US-10-741-600-17661	Sequence 17661, A
C 19	17.8	71.2	2369	20	US-10-739-930-4146	Sequence 4146, Ap
C 20	17.6	70.4	460	10	US-09-918-995-9075	Sequence 9075, Ap
C 21	17.6	70.4	528	19	US-10-767-701-27619	Sequence 27619, A
C 22	17.6	70.4	544	13	US-10-027-632-90568	Sequence 90568, A
C 23	17.6	70.4	544	13	US-10-027-632-304306	Sequence 304306, A
C 24	17.6	70.4	544	17	US-10-027-632-90568	Sequence 90568, A
C 25	17.6	70.4	544	17	US-10-027-632-304306	Sequence 304306, A
C 26	17.6	70.4	605	18	US-10-424-599-65155	Sequence 65155, A
C 27	17.6	70.4	1441	20	US-10-723-860-7987	Sequence 7987, Ap
C 28	17.6	70.4	1994	9	US-09-864-761-4614	Sequence 4614, Ap
C 29	17.6	70.4	2562	14	US-10-237-271-8	Sequence 8, Appli
C 30	17.6	70.4	2562	16	US-10-354-358-13	Sequence 13, Appli
C 31	17.6	70.4	2562	21	US-10-772-636-43	Sequence 43, Appli
C 32	17.6	70.4	2712	17	US-10-104-047-337	Sequence 337, App
C 33	17.6	70.4	2756	17	US-10-388-360-362	Sequence 362, App
C 34	17.6	70.4	2756	21	US-10-956-157-904	Sequence 904, App
C 35	17.6	70.4	3135	19	US-10-437-963-9258	Sequence 9258, Ap
C 36	17.6	70.4	19696	10	US-09-764-891-9327	Sequence 9327, Ap
C 37	17.6	70.4	19696	14	US-10-091-572-874	Sequence 874, App
C 38	17.4	69.6	1152	13	US-10-027-632-118560	Sequence 118560, A
C 39	17.4	69.6	1152	13	US-10-027-632-123821	Sequence 123821, A
C 40	17.4	69.6	1152	13	US-10-027-632-123822	Sequence 123822, A
C 41	17.4	69.6	1152	13	US-10-027-632-123823	Sequence 123823, A
C 42	17.4	69.6	1152	17	US-10-027-632-118560	Sequence 118560, A
C 43	17.4	69.6	1152	17	US-10-027-632-123821	Sequence 123821, A
C 44	17.4	69.6	1152	17	US-10-027-632-123822	Sequence 123822, A
C 45	17.4	69.6	1152	17	US-10-027-632-123823	Sequence 123823, A

ALIGNMENTS

RESULT 1

US-09-294-093B-149/c
; Sequence 149, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700342237H1
US-09-294-093B-149

Query Match 76.8%; Score 19.2; DB 9; Length 270;

Best Local Similarity 62.5%; Pred. No. 46;
Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUCCAGAUAGCCC 25

Db 46 ATCTTCAGCATTCAGATATGACC 23
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RESULT 2
US-10-425-115-117468/c
; Sequence 117468, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 117468
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_38619C.1
US-10-425-115-117468

Query Match 76.8%; Score 19.2; DB 20; Length 597;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 15; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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Db 287 ATCTTCAGCATTCAGATATGACC 264

RESULT 3
US-09-997-722-280/c
; Sequence 280, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 280
; LENGTH: 40304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14527)..(15049)
; OTHER INFORMATION: "n" at position 14527 through 15049 can be any base.
US-09-997-722-280

Query Match 76.8%; Score 19.2; DB 11; Length 40304;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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Db 37678 AACTTGAGGATGCCAGATATATCCC 37655

RESULT 4

US-10-775-169-173/c
; Sequence 173, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William

; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 86574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-173

Query Match 76.8%; Score 19.2; DB 19; Length 86574;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACUUCAGGAUUCAGAUAGCCCC 25
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Db 36754 AACTTGAGGATGCCAGATATATCCC 36731

RESULT 5
US-09-960-352-8669
; Sequence 8669, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8669
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 37-LIB34-021-Q1-E1-B2
US-09-960-352-8669

Query Match 74.4%; Score 18.6; DB 9; Length 391;
Best Local Similarity 64.0%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUUCAGGAUUCAGAUAGCCCC 25
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Db 63 CAATTCGAGTCCAGATGTGCCCC 87

RESULT 6
US-09-960-352-11019
; Sequence 11019, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
US-09-960-352-11019

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; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11019
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 47-LIB34-022-Q1-E1-D4
US-09-960-352-11019

Query Match 74.4%; Score 18.6; DB 9; Length 402;
Best Local Similarity 64.0%; Pred. No. 92;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTUCAGGUAUCCAGAUAGCCCC 25
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Db 315 CAAATTCGGAGTCAGATGTGCC 339

RESULT 7
US-09-960-352-5872
; Sequence 5872, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5872
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (346)...(347)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 25-LIB34-036-Q1-E1-G1
US-09-960-352-5872

Query Match 74.4%; Score 18.6; DB 9; Length 422;
Best Local Similarity 64.0%; Pred. No. 93;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTUCAGGUAUCCAGAUAGCCCC 25
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Db 252 CAAATTCGGAGTCAGATGTGCC 276

RESULT 8
US-10-329-670-1/C
; Sequence 1, Application US/10329670
; Publication No. US20040018503A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,670
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1

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Query Match 74.4%; Score 18.6; DB 17; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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QY 1 CACUUCAGGAUUCGAGUAUGCCC 25
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Db 1071778 CAACTTCAGGATGCCCTTTATGCC 1071754
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RESULT 9

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US-10-158-865-1/c
; Sequence 1, Application US/10158865
; Publication No. US20040203093A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P2C1D1
; CURRENT APPLICATION NUMBER: US/10/158,865
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/557,884
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 08/476,102
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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Query Match 74.4%; Score 18.6; DB 20; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.le+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACUCAGGAUCCAGAUAGCC 25
Db 1071778 CACTTCAGGATGCCCTTATGCCC 1071754

RESULT 10
US-10-981-687-1/c
/ Sequence 1, Application US/10981687
/ Publication No. US20050131222A1
/ GENERAL INFORMATION:
/ APPLICANT: Fleischmann et al.
/ TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
/ FILE REFERENCE: PB186P2CID12
/ CURRENT APPLICATION NUMBER: US/10/981,687
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US 10/159,865
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 09/557,884
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US 08/476,102
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: US 08/426,787
/ PRIOR FILING DATE: 1995-04-21
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1830121
/ TYPE: DNA
/ ORGANISM: Haemophilus Influenzae
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4747)..(4747)
/ OTHER INFORMATION: n equals a,t,c, or g
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; LOCATION: (119924)..(119924)
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; OTHER INFORMATION: n equals a,t,c, or g
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:

Query Match 74.4%; Score 18.6; DB 22; Length 1830121;
Best Local Similarity 64.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACUCCAGGAUCCAGAUAGCCC 25
Db 1071778 CAACUCCAGGAUCCAGGAUAGCCC 1071754
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RESULT 11
US-10-972-079-58889
; Sequence 58889, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 58889
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Chicken 19866894316535_1
US-10-972-079-58889
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Query Match 73.6%; Score 18.4; DB 22; Length 564;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 6 UCAGGAUCCAGAUAGCCC 25
Db 318 TCAGGTTTCAGATATGCC 337
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RESULT 12
US-09-851-682A-2/c
; Sequence 2, Application US/09851682A
; Patent No. US20020091248A1
; GENERAL INFORMATION:
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; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/851,682A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US/09/172,422
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-851-682A-2

Query Match      73.6%; Score 18.4; DB 9; Length 8473;
Best Local Similarity 65.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACUUCAGGAUCCAGAU 21
        |||::|||::: |||:::
DB      1595 AACTTCAGGATACAGATAT 1576

RESULT 13
US-10-893-315-332/c
; Sequence 332, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-332

Query Match      72.0%; Score 18; DB 22; Length 601;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAACUUCAGGAUCCAGA 18
        |||::|||::: |||:::
DB      521 CAACTTCAGGATTCAGA 504

RESULT 14
US-10-893-315-1543/c
; Sequence 1543, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-1543

Query Match      72.0%; Score 18; DB 22; Length 601;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAACUUCAGGAUCCAGA 18
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DB      521 CAACTTCAGGATTCAGA 504

Search completed: July 30, 2005, 15:29:44
Job time : 490.108 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	25	100.0	25	21	US-10-956-157-169389	Sequence 169389,
C 2	25	100.0	75	9	US-09-758-140-7	Sequence 7, Appli
C 3	25	100.0	75	9	US-09-972-599A-7	Sequence 7, Appli
C 4	25	100.0	75	9	US-09-972-599A-23	Sequence 23, Appli
C 5	25	100.0	90	9	US-09-972-599A-25	Sequence 25, Appli
C 6	25	100.0	105	9	US-09-972-599A-27	Sequence 27, Appli
C 7	25	100.0	120	9	US-09-758-140-17	Sequence 17, Appli

SUMMARIES

RESULT 2


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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 10
US-09-972-599A-19/c
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020077295A1o gene
US-09-972-599A-19

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 36 CTGGATAGCTTGGATCACACCCCTTG 12

RESULT 11
US-09-972-599A-21/c
; Sequence 21, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 57
; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
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; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1120
; OTHER INFORMATION: of human No. US20020077295A1oA
US-09-972-599A-21

Query Match      100.0%; Score 25; DB 9; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 12
US-10-327-213-10/c
; Sequence 10, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-327-213-10

Query Match      100.0%; Score 25; DB 19; Length 198;
Best Local Similarity 72.0%; Pred. No. 0.045;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUGGAUAGCUUGGAUCACACCCUUG 25
Db 33 CTGGATAGCTTGGATCACACCCCTTG 9

RESULT 13
US-10-660-946-9/c
; Sequence 9, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/660,946
;; FILING DATE: 12-Sep-2003
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/228,213A
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 08/700,607
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0114 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 261 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; IMMEDIATE SOURCE:
;; LIBRARY: SPLNFET01
;; CLONE: 28742
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-660-946-9

Query Match 100.0%; Score 25; DB 18; Length 261;
Best Local Similarity 72.0%; Pred. No. 0.046;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
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Db 124 CTGGATAGCTTGGATCACACCCCTTG 100

RESULT 14

US-10-956-157-9764/c
;; Sequence 9764, Application US/10956157
;; Publication No. US20050118625A1
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Mounts, William
;; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;; FILE REFERENCE: 031896-043000 (AM 101081)
;; CURRENT APPLICATION NUMBER: US/10/956,157
;; CURRENT FILING DATE: 2004-10-04
;; NUMBER OF SEQ ID NOS: 319805
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 9764
;; LENGTH: 600
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-956-157-9764

Query Match 100.0%; Score 25; DB 21; Length 600;
Best Local Similarity 72.0%; Pred. No. 0.051;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
|:|||||:|||||:|||||:|
Db 216 CTGGATAGCTTGGATCACACCCCTTG 192

RESULT 15

US-09-880-107-3484/c
;; Sequence 3484, Application US/09880107

;; Patent No. US20020142981A1
;; GENERAL INFORMATION:
;; APPLICANT: Horne, Darci T.
;; APPLICANT: Vockley, Joseph G.
;; APPLICANT: Scherf, Uwe
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;; FILE REFERENCE: 44921-5028-WO
;; CURRENT APPLICATION NUMBER: US/09/880,107
;; CURRENT FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: US 60/211,379
;; PRIOR FILING DATE: 2000-06-14
;; PRIOR APPLICATION NUMBER: US 60/237,054
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 3950
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3484
;; LENGTH: 639
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023
;; NAME/KEY: unsure
;; LOCATION: (1)..{639}
;; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3484

Query Match 100.0%; Score 25; DB 9; Length 639;
Best Local Similarity 72.0%; Pred. No. 0.052;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUGGAUAGCUUGGAUACACCCUUG 25
|:|||||:|||||:|||||:|
Db 415 CTGGATAGCTTGGATCACACCCCTTG 391

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Job time : 484.108 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2005, 15:15:15 ; Search time 1307 Seconds
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11092.639 Million cell updates/sec

Title: US-09-544-776-1

Perfect score: 2240

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2231	99.6	2235	14	US-10-060-036-54
2	2191	97.8	2226	21	US-10-060-036-54
3	1908	85.2	2050	21	US-10-060-036-54
4	1892.8	84.5	2052	19	US-10-060-036-54
5	1892.8	84.5	2052	22	US-10-060-036-54
6	1607.4	71.8	1610	9	US-09-765-205-5
7	1607.4	71.8	1610	21	US-10-347-669-5

8	1488.8	66.5	1798	19	US-10-466-258-10	Sequence 10, Appl
9	1488.8	66.5	1798	22	US-10-466-258-10	Sequence 10, Appl
10	1473.4	65.8	1514	9	US-09-823-245A-349	Sequence 349, Appl
11	1409	62.9	4632	14	US-10-060-036-53	Sequence 53, Appl
12	1370	61.2	1609	21	US-10-060-036-53	Sequence 4527, Ap
13	1369	61.1	1400	21	US-10-060-036-53	Sequence 4527, Ap
14	1369	61.1	1400	21	US-10-060-036-53	Sequence 4527, Ap
15	1359.2	60.7	1785	17	US-10-439-388-62	Sequence 62, Appl
16	1359.2	60.7	1785	21	US-10-439-388-62	Sequence 62, Appl
17	1299	58.0	1400	21	US-10-060-036-53	Sequence 1705, Ap
18	1299	58.0	1400	21	US-10-060-036-53	Sequence 1705, Ap
19	1258	56.2	1400	21	US-10-060-036-53	Sequence 1705, Ap
20	1122	50.1	1122	9	US-09-789-386-5	Sequence 5, Appli
21	1097.6	49.0	2610	18	US-10-641-643-382	Sequence 382, App
22	1057	47.2	2782	15	US-10-205-194-165	Sequence 165, App
23	1010.2	45.1	4710	10	US-09-764-891-7385	Sequence 7385, Ap
24	910	40.6	1160	14	US-10-175-523-156	Sequence 156, App
25	907	40.5	4053	9	US-09-758-140-5	Sequence 5, Appli
26	907	40.5	4053	9	US-09-758-140-5	Sequence 5, Appli
27	907	40.5	4053	19	US-10-717-597-310	Sequence 110, App
28	906.8	40.5	994	11	US-09-978-360A-110	Sequence 110, App
29	904.2	40.4	1980	17	US-10-220-891-22	Sequence 22, Appl
30	902	40.3	972	17	US-10-437-931-1	Sequence 1, Appli
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33	751.8	33.6	4684	9	US-09-833-348-17	Sequence 4528, Ap
34	751.8	33.6	4684	20	US-10-810-653-17	Sequence 17, Appl
35	682	30.4	799	18	US-10-660-946-2	Sequence 17, Appl
36	610.4	27.2	3413	13	US-10-001-843-61	Sequence 2, Appli
37	610.4	27.2	3413	23	US-11-005-609-61	Sequence 61, Appl
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41	565.4	25.2	3579	9	US-09-789-386-1	Sequence 22, Appl
42	565.4	25.2	3579	18	US-10-267-502-212	Sequence 212, App
43	565.4	25.2	3579	19	US-10-327-213-8	Sequence 8, Appli
44	565.4	25.2	3579	19	US-10-466-258-8	Sequence 8, Appli
45	565.4	25.2	3579	20	US-10-810-653-22	Sequence 22, Appl

ALIGNMENTS

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US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugui
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54

Query Match 99.6%; Score 2231; DB 14; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Q _y	181	GCCACACCCCGCGCAGACCGCTTCAAGTACCAAGTTCGTCGAGGAGCCCGAGGACGAGG	240
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Q _y	241	AGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACTTGGAGGAGCTGGAGGTGC	300
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Q _y	361	CGCGCCCTCTGATGGACTTTCGGAAATGACTTGTGTGCGCGCGCGCCCGGGGAGCCCTGC	420
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Q _y	481	CGACCGTCGCCGCGCATTCCCGCTGTCTGTGCGGAGTCTGCGCTTCAAGCTCCCTG	540
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Qy 2046 CTGAATCTAATGCTTCCAAAATGTTGTTTGGCAAAATATCAAACTTTGTTATGCAAG 2105
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US-09-765-205-5
; Sequence 5, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765.205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212.440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-09-765-205-5
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Query Match 71.8%; Score 1607.4; DB 9; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 187 CCGCGCGCAGCCCGGCTTCAAGTACAGTTCTGAGGGAGCCCGGAGGAGGAGGAAG 246
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Db 301 GGAAGCCCGCGCGCGGCTGTCCGCGGCCCGCAGTGTCCACCGCCCTCGCGCGCGCGCGC 360
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US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5
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Query Match 71.8%; Score 1607.4; DB 21; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 CACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCCCAACCCCAACAA 60
QY 67 CCGCCCGCGGCTCTGAGACGCGGCCCGCGCGCGCGCGCGCGCGCGCATCTCC 126
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Db 121 ACCCTCAGCCATGGAAGACCTGGAACAGTCTCTCTGGTCTCTGCTCGGACGCCAC 180
QY 187 CCCGCGCGCAGCCCGGTTCAAGTACCAAGTTCTGAGGAGCCCGAGGACGAGGAGAG 246
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Db 601 CCGGTGGAACCCCGAGCCCGGCTCCCGCGCGCGCCCTCCACCCCGCGCGCGCCCA 660
Qy 667 AGCCGAGGGGCTCTCGGGCTCAGTGGTGTGTGACCTCTCTGACTGAGAGACATTAAGA 726
Db 661 AGCCGAGGGGCTCTCGGGCTCAGTGGTGTGTGACCTCTCTGACTGAGAGACATTAAGA 720
Qy 727 AGACTGAGTGGTGTGGTGCCAGCCCTATTCCTGCTGCTTTCATGACAGTATTCAGCA 786
Db 721 AGACTGAGTGGTGTGGTGCCAGCCCTATTCCTGCTGCTTTCATGACAGTATTCAGCA 780
Qy 787 TTGTGAGGTGAACGCTACATTCGCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGA 846
Db 781 TTGTGAGGTGAACGCTACATTCGCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGA 840
Qy 847 TATCAAGGGTGTGATCAAGCTATCAAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 906
Db 841 TATCAAGGGTGTGATCAAGCTATCAAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 900
Qy 907 ATCTGGAATCTGAAGTGTCTATATCTGAGGAGTGGTTCAGAAGTACAGTAATTCCTC 966
Db 901 ATCTGGAATCTGAAGTGTCTATATCTGAGGAGTGGTTCAGAAGTACAGTAATTCCTC 960
Qy 967 TTGCTCATGTGAACGACGATGAAGAACTCAGCGCGCTCTTCTTAGTTGATGATTTAG 1026
Db 961 TTGCTCATGTGAACGACGATGAAGAACTCAGCGCGCTCTTCTTAGTTGATGATTTAG 1020
Qy 1027 TTGATCTCTGAAGTTTGACGTGTGATGGGTATTTACCTATGTTGGTCCCTGTTTA 1086
Db 1021 TTGATCTCTGAAGTTTGACGTGTGATGGGTATTTACCTATGTTGGTCCCTGTTTA 1080
Qy 1087 ATGCTCTGACACTACTGATTTGGCTCTCAFTTCACTCTTCAGTGTTCCTGTTATTTATG 1146
Db 1081 ATGCTCTGACACTACTGATTTGGCTCTCAFTTCACTCTTCAGTGTTCCTGTTATTTATG 1140
Qy 1147 AACGGCATCAGGCACAGATAGATCATTTCTAGGACTTGCAAAATGAAGATGTTAAAGATG 1206
Db 1141 AACGGCATCAGGCACAGATAGATCATTTCTAGGACTTGCAAAATGAAGATGTTAAAGATG 1200
Qy 1207 CTATGGCTTAAATCCAGCAAAATCCCTGGATTTGAAGCGCAAGAGCTGAATGAAGACGCC 1266
Db 1201 CTATGGCTTAAATCCAGCAAAATCCCTGGATTTGAAGCGCAAGAGCTGAATGAAGACGCC 1260
Qy 1267 CAAATAATTAAGTAGGAGTTCATCTTTAAAGGGATATTCATTTGATTAATACCGGGGAGG 1326
Db 1261 CAAATAATTAAGTAGGAGTTCATCTTTAAAGGGATATTCATTTGATTAATACCGGGGAGG 1320
Qy 1327 GTCAGGGAAGAACGAACTTGACGCTGTCAGTGCAGTTCACAGATCGTGTGTAGATCTTT 1386
Db 1321 GTCAGGGAAGAACGAACTTGACGCTGTCAGTGCAGTTCACAGATCGTGTGTAGATCTTT 1380
Qy 1387 ATTTTGTAGCCATGACCTGCTGTGAGGAAATATACCTGTCTTGACTGCGATGCTGTCATC 1446
Db 1381 ATTTTGTAGCCATGACCTGCTGTGAGGAAATATACCTGTCTTGACTGCGATGCTGTCATC 1440
Qy 1447 ATCTTAAGTATTTGAAGCTGCTATGTATGATTTAAACCGTAATCATATCTTTTCCCTAT 1506
Db 1441 ATCTTAAGTATTTGAAGCTGCTATGTATGATTTAAACCGTAATCATATCTTTTCCCTAT 1500
Qy 1507 CTGAGGCACCTGGTGAATAAAAAACCTGTATATTTTACTTTGTTGTCAGATAGTCTTGCGG 1566
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Db 1501 CTGAGGCACCTGGTGGATATAAAAAACCTGTATATTTTACTTTGTCAGATAGTCTTGCGG 1560
Qy 1567 CATCTTGGCAAGTTGCGAGAGATGGTGAGCTAGAAAAAATAAAAAA 1615
Db 1561 CATCTTGGCAAGTTGCGAGAGATGGTGAGCTAGAAAAAATAAAAAA 1609

RESULT 8
US-10-466-258-10
; Sequence 10, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-258-10

Query Match 66.5%; Score 1488.8; DB 19; Length 1798;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;

Qy 692 GGTGTTTGACCTCTCTGACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 751
Db 247 GGTGTTTGACCTCTCTGACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 306
Qy 752 CTTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTC 811
Db 307 CTTATTCCTGCTGCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTC 366
Qy 812 CTTGGCCCTCTCTCTGACCATCAGCTTTAGATATACAAGGGTGTGATCCAGGCTAT 871
Db 367 CTTGGCCCTCTCTCTGACCATCAGCTTTAGATATACAAGGGTGTGATCCAGGCTAT 426
Qy 872 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 931
Db 427 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 486
Qy 932 TGAGGAGTTGGTTCAGAAATACAGTAATTCGTCTTTGGTCATGTGAATCTGCACGATAAA 991
Db 487 TGAGGAGTTGGTTCAGAAATACAGTAATTCGTCTTTGGTCATGTGAATCTGCACGATAAA 546
Qy 992 GGAACCTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTGT 1051
Db 547 GGAACCTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTGT 606
Qy 1052 GATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db 607 GATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTGGC 666
Qy 1112 TCTCATTTCACTCTTCAAGTGTTCCTGTTATTTAATGAACCGGCATCAGGACAGATAGATC 1170
Db 667 TCTCATTTCACTCTTCAAGTGTTCCTGTTATTTAATGAACCGGCATCAGGACAGATAGATC 725
Qy 1171 ATTATCTAGGACTTGCAAAATGAAGATGTTAAAGTGTCTATGGCTTAAATCCAGCAAAA 1230
Db 726 ATTATCTAGGACTTGCAAAATGAAGATGTTAAAGTGTCTATGGCTTAAATCCAGCAAAA 785
Qy 1231 TCCTGGAATGAAGCGCAAAAGCTGAATGAAACCGCCCAAAATTAATTAAGTAGGAGTTATC 1290
Db 786 TCCTGGAATGAAGCGCAAAAGCTGAATGAAACCGCCCAAAATTAATTAAGTAGGAGTTATC 845
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QY 1291 TTTAAAGGGATATTCAATTGATTAATACGGGGAGGGTCAGGGAAGAACGAACTTTGACG 1350
Db 846 TTTAAAGGGATATTCAATTGATTAATACGGGGAGGGTCAGGGAAGAACGAACTTTGACG 905
QY 1351 TTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCATGCATGTTGTA 1410
Db 906 TTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTAGCCATGCATGTTGTA 965
QY 1411 GGAAAAATTTACCTGCTTTGACTGCCATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1470
Db 966 GGAAAAATTTACCTGCTTTGACTGCCATGTTTTCATCATCTTAAAGTATTGTAAGCTGCTAT 1025
QY 1471 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGTTGGAATAA 1526
Db 1026 GTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGTTGGAATAA 1085
QY 1527 AAAACCTGTATATTTTACTTTGTTGACATAGTCTTGCGGCACTCTTGGAAGTTGCAGAG 1586
Db 1086 AAAACCTGTATATTTTACTTTGTTGACATAGTCTTGCGGCACTCTTGGAAGTTGCAGAG 1145
QY 1587 ATGGTGGAGCTAGAAAAAAGGCTTTTTCAGTTTGTGCACTGTTGATGTC 1646
Db 1146 ATGGTGGAGCTAGAAAAAAGGCTTTTTCAGTTTGTGCACTGTTGATGTC 1205
QY 1647 CGTGTAGATTGATGAGATTTTCTGAAATGAAGTTTGTGTTTGTAGACGATCATACCGGT 1706
Db 1206 CGTGTAGATTGATGAGATTTTCTGAAATGAAGTTTGTGTTTGTAGACGATCATACCGGT 1265
QY 1707 AAAGCAGGAATGACAAAGCTTCTTCTGTTATGTTCTAGTGTATTTGTGACTTTTACT 1766
Db 1266 AAAGCAGGAATGACAAAGCTTCTTCTGTTATGTTCTAGTGTATTTGTGACTTTTACT 1325
QY 1767 GTTATATTAATTTGCAATTAAGTAAATATAGTATATATATGATAGTGTTCACAAAGC 1826
Db 1326 GTTATATTAATTTGCAATTAAGTAAATATAGTATATATATGATAGTGTTCACAAAGC 1385
QY 1827 TTAGACCTTTTACCTTCCAGCCACCCACAGTCTTTGATATTTTCAGAGTCAGTCAATTGGTT 1886
Db 1386 TTAGACCTTTTACCTTCCAGCCACCCACAGTCTTTGATATTTTCAGAGTCAGTCAATTGGTT 1445
QY 1887 ATACATGTGTAGTTCCAAAGCACAATAGCTAGAGAAAGAAATATTTCTAGAGCACTACC 1946
Db 1446 ATACATGTGTAGTTCCAAAGCACAATAGCTAGAGAAAGAAATATTTCTAGAGCACTACC 1505
QY 1947 ATCTGTTTTCAACATGAATGCCACACATAGAACTCCAAACATCAATTTTCATTGCA 2006
Db 1506 ATC-GTTTTCAACATGAATGCCACACATAGAACTCCAAACATCAATTTTCATTGCA 1564
QY 2007 CAGACTGACTGTAGTTAAATTTTGTACAGAAATCTATGGAATCTTAATGCTTCCAAAA 2066
Db 1565 CAGACTGACTGTAGTTAAATTTTGTACAGAAATCTATGGAATCTTAATGCTTCCAAAA 1624
QY 2067 ATGTTGTTTGTGGAATATCAAAATGTTATGCAAGAAATTTAATTTACAAAATGA 2126
Db 1625 ATGTTGTTTGTGGAATATCAAAATGTTATGCAAGAAATTTAATTTACAAAATGA 1684
QY 2127 AGATTTATACCAATCTGTGTTTAAAGCTGTACTGAACCTAAATCTGTGGAATGCTGAAC 2186
Db 1685 AGATTTATACCAATCTGTGTTTAAAGCTGTACTGAACCTAAATCTGTGGAATGCTGAAC 1744
QY 2187 TGTAAAGCAAGTATCAATTAAGCTTTATAGACTTTAAAAAAGGCTTTGGAATGCTGAAC 2240
Db 1745 TGTAAAGCAAGTATCAATTAAGCTTTATAGACTTTAAAAAAGGCTTTGGAATGCTGAAC 1798
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RESULT 9

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US-10-466-391A-10
; Sequence 10, Application US/10466391A
; Publication No. US20040146953A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
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; CURRENT APPLICATION NUMBER: US/10/466.391A
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-391A-10
```

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Query Match      66.5%; Score 1488.8; DB 22; Length 1798;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 7; Indels 7; Gaps 4;

QY 692 GGTGTTGACCTCTCTGTACTGAGAGACATTTAAGAAGACTGAGTGGTGTGGTGGCCAG 751
Db 247 GGTGTTGACCTCTCTGTACTGAGAGACATTTAAGAAGACTGAGTGGTGTGGTGGCCAG 306
QY 752 CCTATTCTCTGCTCTTTCATTTGACAGATTTTCTGAGCGTAAACAGCCTACATGTC 811
Db 307 CCTATTCTCTGCTCTTTCATTTGACAGATTTTCTGAGCGTAAACAGCCTACATGTC 366
QY 812 CTGCCCCCTGCTCTCTGTGACCATCAGCTTTTGGATATACAAAGGCTGTGATCCAAAGCTAT 871
Db 367 CTGCCCCCTGCTCTCTGTGACCATCAGCTTTTGGATATACAAAGGCTGTGATCCAAAGCTAT 426
QY 872 CCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTGTCTATATC 931
Db 427 CCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTGTCTATATC 486
QY 932 TGAGGAGTTGGTTTCTGAGTACAGTAAATCTGCTCTTGGTCTATCTGAAAGTGTGCACTGATAA 991
Db 487 TGAGGAGTTGGTTTCTGAGTACAGTAAATCTGCTCTTGGTCTATCTGAAAGTGTGCACTGATAA 546
QY 992 GGAATCTAGGGCGCTCTTCTTGTAGTTGATGATTTAGTTAGTTCTCTGAAAGTGTGCACTGATAA 1051
Db 547 GGAATCTAGGGCGCTCTTCTTGTAGTTGATGATTTAGTTAGTTCTCTGAAAGTGTGCACTGATAA 606
QY 1052 GATGTGGGTATTTACTTATGTTGGTCTGTTTAAAGTCTGACACTTCTGATTTTGGC 1111
Db 607 GATGTGGGTATTTACTTATGTTGGTCTGTTTAAAGTCTGACACTTCTGATTTTGGC 666
QY 1112 TCTCAATTTCACT-CTTCAGTCTTCTGTTTATTTATGAAAGGCTAGGCACTAGATATC 1170
Db 667 TCTCAATTTCACTCTCTTCACTGTTCTCTGTTATTTA-GAACGGGATCAGGCACTAGATATC 725
QY 1171 ATTATCTAGGACTTTCGAAATTAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAAA 1230
Db 726 ATTATCTAGGACTTTCGAAATTAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAAA 785
QY 1231 TCCCTGGAATGAAGCGCAAAAGCTGAAATGAACCGCCAAAAATAATTTAGTAGAGTTTCATC 1290
Db 786 TCCCTGGAATGAAGCGCAAAAGCTGAAATGAACCGCCAAAAATAATTTAGTAGAGTTTCATC 845
QY 1291 TTTAAAGGGGATATTTCAATTTGATTTATAGCGGGGAGGGTCAGGGAAGAACCACTTGGAG 1350
Db 846 TTTAAAGGGGATATTTCAATTTGATTTATAGCGGGGAGGGTCAGGGAAGAACCACTTGGAG 905
QY 1351 TTGAGTGCAGTTTTCACAGATCGTTTGTAGATCTTTATTTTAGCCATGCATGTTGTA 1410
Db 906 TTGAGTGCAGTTTTCACAGATCGTTTGTAGATCTTTATTTTAGCCATGCATGTTGTA 965
QY 1411 GGAAAAATTTACCTGCTTTGACTGCCATGTTGTTTCATCTTAAAGTATTGTAAGCTGCTAT 1470
Db 966 GGAAAAATTTACCTGCTTTGACTGCCATGTTGTTTCATCTTAAAGTATTGTAAGCTGCTAT 1025
QY 1471 GTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGTTGGAATAA 1526
Db 1026 GTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGTTGGAATAA 1085
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Db 961 TGTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTTTCTGGTA 1020
QY 1740 TGTTCTAGGTGATTGTGACATTTTACTGCTTATTAATTAATGCGCAATATAAGTAAATATAGA 1799
Db 1021 TGTCTAGGTGATTGTGACATTTTACTGCTTATTAATTAATGCGCAATATAAGTAAATATAGA 1080
QY 1800 TTATATATGTATAGTGTGTTTCAAAAGCTTAGACCTTTTACCTTTCAGCCACCCACAGTGC 1859
Db 1081 TTATATATGTATAGTGTGTTTCAAAAGCTTAGACCTTTTACCTTTCAGCCACCCACAGTGC 1140
QY 1860 TTGATATTTTCAGTCACTCATTTGGTTATATACATGCTGTAGTTTCCAAAGCACAATAAGCTAGA 1919
Db 1141 TTGATATTTTCAGTCACTCATTTGGTTATATACATGCTGTAGTTTCCAAAGCACAATAAGCTAGA 1200
QY 1920 AGAAGAAATATTTTCAGGAGCACTACCATCTGTTTCAACATGAAATGCCACACACATAG 1979
Db 1201 AGAAGAAATATTTTCAGGAGCACTACCATCTGTTTCAACATGAAATGCCACACACATAG 1260
QY 1980 AACTCCAAACATCAATTTCAATTGACAGACTGACTGTAGTTAATTTTGTACAGAAATC 2039
Db 1261 AACTC- --CAACATCAATTTCAATTGACAGACTGACTGTAGTTAATTTTGTACAGAAATC 1317
QY 2040 TATGACATGAATCTAATGCTTCCAAAATGTTTGTGTTTGGCAATATCAACATTTGTTA 2099
Db 1318 TATGACATGAATCTAATGCTTCCAAAATGTTTGTGTTTGGCAATATCAACATTTGTTA 1377
QY 2100 TGCAAGAAATATTAATTAATTAACAAATGAAGATTTATACCATTTGTGTTTAAAGCTGACTGA 2159
Db 1378 TGCAAGAAATATTAATTAATTAACAAATGAAGATTTATACCATTTGTGTTTAAAGCTGACTGA 1437
QY 2160 ACTAATCTGTGGAATGCAATGTGAACCTGTAAAGCAAAAGATATCAATAAAGCTTATAGAC 2219
Db 1438 ACTAATCTGTGGAATGCAATGTGAACCTGTAAAGCAAAAGATATCAATAAAGCTTATAGAC 1497
QY 2220 TTAATAAAAAAAAAAAAAA 2236
Db 1498 GTAAAAAAACTTAGAAA 1514

RESULT 11
US-10-060-036-53
; Sequence 53, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

Query Match 62.9%; Score 1409; DB 14; Length 4632;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1479; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 693 GTTGTGACCTCCTGCTACTGGAGACACATTAAGAGACTGGAGTGGTGTGTTGGTCCAGC 752
Db 3154 GTTGTGACCTCCTGCTACTGGAGACACATTAAGAGACTGGAGTGGTGTGTTGGTCCAGC 3213
QY 753 CTATTCCTGCTGCTTTTCATTTGACGATATTCAGACTTTGTGAGCGTAAACGCCTACATTGCC 812
Db 3214 CTATTCCTGCTGCTTTTCATTTGACGATATTCAGACTTTGTGAGCGTAAACGCCTACATTGCC 3273
QY 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 872
Db 3274 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 3333
QY 873 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 932
Db 3334 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 3393
QY 933 GAGAGTTGGTTTCAAGATACAGTAATTCCTCTCTTGGTCATGTGAACGACGATTAAG 992
Db 3394 GAGAGTTGGTTTCAAGATACAGTAATTCCTCTCTTGGTCATGTGAACGACGATTAAG 3453
QY 993 GAACTCAGGCCCTCTCTTCTAGTTTGAATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 1052
Db 3454 GAACTCAGGCCCTCTCTTCTAGTTTGAATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 3513
QY 1053 ATGCGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1112
Db 3514 ATGCGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 3573
QY 1113 CTGATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 3574 CTGATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT 3633
QY 1173 TATCTAGGACTTGCATAATGAAGATGTTTAAAGATGCTATGGCTTAAATCAAGCAAAAAATC 1232
Db 3634 TATCTAGGACTTGCATAATGAAGATGTTTAAAGATGCTATGGCTTAAATCAAGCAAAAAATC 3693
QY 1233 CTGGAATGAAGCGCAAGCTGGAATGAAGCGCAAAATTAATTAGTAGGAGTTTCATCTT 1292
Db 3694 CTGGAATGAAGCGCAAGCTGGAATGAAGCGCAAAATTAATTAGTAGGAGTTTCATCTT 3753
QY 1293 TAAAGGGGATATTCATTTGATTTATACGGGGGAGGGTCAGGGAAGAACGAACTTGACGTT 1352
Db 3754 TAAAGGGGATATTCATTTGATTTATACG----- 3780
QY 1353 GCAGTGCAATTTTCACAGATCGTTGTAGATCTTTATTTTAGCCATGCACTGTTGTGAGG 1412
Db 3781 -----GAUCTTTATTTTAGCCATGCACTGTTGTGAGG 3813
QY 1413 AAAAAATACCTGTCTGTGATGCCATGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGT 1472
Db 3814 AAAAAATACCTGTCTGTGATGCCATGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGT 3873
QY 1473 ATGGATTTAAACCGTAATCATCTTTTCTCTATCTGAGGCACCTGGTGAATTAAGAAC 1532
Db 3874 ATGGATTTAAACCGTAATCATCTTTTCTCTATCTGAGGCACCTGGTGAATTAAGAAC 3933
QY 1533 TGTATATTTTACTTTTGTGACATAGTCTTCCGCTCTTCCGCAAGTTGCAAGATGCTG 1592
Db 3934 TGTATATTTTACTTTTGTGACATAGTCTTCCGCTCTTCCGCAAGTTGCAAGATGCTG 3993
QY 1593 GAGCTAGAAAAAAGGCTTTTTCAGTTTGTGACCTGCTGTATGCTGCGTGTGTA 1652
Db 3994 GAGCTAGAAAAAAGGCTTTTTCAGTTTGTGACCTGCTGTATGCTGCGTGTGTA 4053
QY 1653 GATTGATGACAGATTTTCTGAAATGAATGTTTGTGTTAGACAGATCATACCGTAAAGCA 1712
Db 4054 GATTGATGACAGATTTTCTGAAATGAATGTTTGTGTTAGACAGATCATACCGTAAAGCA 4113
QY 1713 GGAATGACAAAGCTTGTCTGTTTCTAGTGTGTTTGTGACCTTTTACTGTTATA 1772
Db 4114 GGAATGACAAAGCTTGTCTGTTTCTAGTGTGTTTGTGACCTTTTACTGTTATA 4173
QY 1773 TTAATTTGCAATATAAGTAAATATAGATTTATATATGATGTTTCAAAAGCTTAGAC 1832
Db 4174 TTAATTTGCAATATAAGTAAATATAGATTTATATATGATGTTTCAAAAGCTTAGAC 4233
QY 1833 CTTTACCTTCCAGCCACCCACAGTGTGATTTTCAAGACTCAGTCACTGTTGTTATACAT 1892
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Db 4234 CTTTACCTTCCAGCCACCCACAGTGTGTGATATTTTCAGAGTCAGTCATTGGTTATACAT 4293
Qy 1893 GTGTAGTTCGAAGCACATAGCTAGAGAGAAATATTTCTAGGAGCAGTACCATCTGT 1952
Db 4294 GTGTAGTTCGAAGCACATAGCTAGAGAGAAATATTTCTAGGAGCAGTACCATCTGT 4353
Qy 1953 TTTCAACATGAATGAGCCACACACATAGAACTCCAAACACATCAATTTTCATTGACAGACT 2012
Db 4354 TTTCAACATGAATGAGCCACACACATAGAACTCCAAACACATCAATTTTCATTGACAGACT 4413
Qy 2013 GACTGTAGTTAATTTGTGCAGAACTCTATGAGCTGAATCTAAATGCTTCCAAAAATGTTG 2072
Db 4414 GACTGTAGTTAATTTGTGCAGAACTCTATGAGCTGAATCTAAATGCTTCCAAAAATGTTG 4473
Qy 2073 TTTGTTTGCAAAATATCAAACTGTTATGCAAGAAATTTAAATACAAATGAAGATTT 2132
Db 4474 TTTGTTTGCAAAATATCAAACTGTTATGCAAGAAATTTAAATACAAATGAAGATTT 4533
Qy 2133 ATACCATTTGGTTTAAAGCTGTACTGAACATAAATCTGTGGAATGCATTTGTGAACGTAAA 2192
Db 4534 ATACCATTTGGTTTAAAGCTGTACTGAACATAAATCTGTGGAATGCATTTGTGAACGTAAA 4593
Qy 2193 AGCAAGTATCAATAAAGCTTTATAGACTTTAAAAAATAA 2231
Db 4594 AGCAAGTATCAATAAAGCTTTATAGACTTTAAAAAATAA 4632

RESULT 12
US-10-956-157-4527
; Sequence 4527, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4527
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4527

Query Match 61.2%; Score 1370; DB 21; Length 1609;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 67; Gaps 3;

Qy 692 GGTGTTTGACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAG 751
Db 139 GGTGTTTGACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAG 198
Qy 752 CCTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAAACAGCTACATGTC 811
Db 199 CCTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAAACAGCTACATGTC 258
Qy 812 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 871
Db 259 CTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 318
Qy 872 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATGCTATATC 931
Db 319 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATGCTATATC 378
Qy 932 TGAGGAGTGGTTTCAAGATACAGTAAATTCGCTCTTGGTCATGTAAGTGAATGCAAGTAAA 991
Db 379 TGAGGAGTGGTTTCAAGATACAGTAAATTCGCTCTTGGTCATGTAAGTGAATGCAAGTAAA 438
Qy 992 GGAACCTAGGGCCCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAGTTTGAGTGT 1051

Db 439 GGAACCTAGGGCCCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAGTTTTCAGTGT 498
Qy 1052 GATGTGGGTATTTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db 499 GATGTGGGTATTTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 558
Qy 1112 TCTCATTTCCTCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1171
Db 559 TCTCATTTCCTCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 618
Qy 1172 TTATCTAGGACTTTCGCAATTAAGAAATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAA 1231
Db 619 TTATCTAGGACTTTCGCAATTAAGAAATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAA 678
Qy 1232 CCCTGGATTTGAAGCGCAAAAGCTGAATGAAACCGCCAAAAATTAATAGTAGGAGTTTCATCT 1291
Db 679 CCCTGGATTTGAAGCGCAAAAGCTGAATGAAACCGCCAAAAATTAATAGTAGGAGTTTCATCT 738
Qy 1292 TTAAGGGGATATTTCAATTTGATTTATACGGGGGAGGGTCAGGGAAGAACGACCTTTGACGT 1351
Db 739 TTAAGGGGATATTTCAATTTGATTTATACGGGGGAGGGTCAGGGA----- 781
Qy 1352 TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTAGCCATGCACTGTTGTGAG 1411
Db 782 -----CCATGCACTGTTGTGAG 798
Qy 1412 GAAAAATTAATCTGTCTTGAATGCAATGTTTCAATCTTAAGTATTTGTAAGCTGCTATG 1471
Db 799 GAAAAATTAATCTGTCTTGAATGCAATGTTTCAATCTTAAGTATTTGTAAGCTGCTATG 858
Qy 1472 TATGGATTTAAACCGTAATCATATCTTTTCCATCTATCTCTGAGGCACTGGTGGAAATAA 1527
Db 859 TATGGATTTAAACCGTAATCATATCTTTTCCATCTATCTCTGAGGCACTGGTGGAAATAA 918
Qy 1528 AAACCTGTATATTTTACTTTGTCAGATAGTCTTGGCGCATCTTGCGAAGTTTCAGAGA 1587
Db 919 AAACCTGTATATTTTACTTTGTCAGATAGTCTTGGCGCATCTTGCGAAGTTTCAGAGA 978
Qy 1588 TGTGTGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTGTATGTTCC 1647
Db 979 TGTGTGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTGTATGTTCC 1038
Qy 1648 GTGTAGATTTGATGAGATTTTCTGAAATGAATGTTTGTAGGAGATCATACCGGTA 1707
Db 1039 GTGTAGATTTGATGAGATTTTCTGAAATGAATGTTTGTAGGAGATCATACCGGTA 1098
Qy 1708 AAGCAGGAATGACAAAGCTTTGCTTTCTGATGATGTTCTAGGTGATTTGTGACTTTTACTG 1767
Db 1099 AAGCAGGAATGACAAAGCTTTGCTTTCTGATGATGTTCTAGGTGATTTGTGACTTTTACTG 1158
Qy 1768 TTATATTAATTTGCCAATATAGTAAATATAGATTTATATATGATGATGATTTTTCACAAAGCT 1827
Db 1159 TTATATTAATTTGCCAATATAGTAAATATAGATTTATATATGATGATGATTTTTCACAAAGCT 1218
Qy 1828 TAGACCTTTTACCTTCCAGCCACCCACAGTGTGATTTTTCAGAGTCAGTCAATGTTTA 1887
Db 1219 TAGACCTTTTACCTTCCAGCCACCCACAGTGTGATTTTTCAGAGTCAGTCAATGTTTA 1278
Qy 1888 TAGATGTTAGTTTCCAAAGCACATTAAGCTAGAAAGAAATATTTCTAGGAGCACTACCA 1947
Db 1279 TAGATGTTAGTTTCCAAAGCACATTAAGCTAGAAAGAAATATTTCTAGGAGCACTACCA 1338
Qy 1948 TCTGTTTTCACATGAAATGCCACACATAGAACTCCAAACACATCAATTTTCAATGCTTCAAAA 2007
Db 1339 TCTGTTTTCACATGAAATGCCACACATAGAACTC-----CAACATCAATTTTCAATGCTC 1395
Qy 2008 AGACTGACTGTAGTTAAATTTTGTGACAGAAATCTATGGAATGAAATCTTAATGCTTCAAAA 2067
Db 1396 AGACTGACTGTAGTTAAATTTTGTGACAGAAATCTATGGAATGAAATCTTAATGCTTCAAAA 1455
Qy 2068 TGTGTTTGTGTTTCCAAATATCAACATGTTTATGCAAGAAATTTATTAATTTACAAATGAA 2127
Db 1456 TGTGTTTGTGTTTCCAAATATCAACATGTTTATGCAAGAAATTTATTAATTTACAAATGAA 1515

Qy	2128	GATTATACCATGTGTTTAAAGCTGACTGAATAAATCTGTGGAAATCAATGTGAAC	2187
Db	1516	GAATTAACCATGTGCTTTAAAGCTGACTGAATAAATCTGTGGAAATCAATGTGAAC	1575
Qy	2188	GTAAAACCAAGATATCAATAAGCCTATAGACTT	2221
Db	1576	GTAAAACCAAGATATCAATAAGCCTATAGACTT	1609

RESULT 13
US-10-956-157-9766
; Sequence 9766, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9766
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9766

		Query Match	61.1%; Score 1369; DB 21; Length 1400;
		Best Local Similarity	99.5%; Pred. No. 0;
		Matches 1396; Conservative	0; Mismatches 0; Indels 7; Gaps 2;

Qy	823	TCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTCACCAAGCTATCCAGAATACAG	882
Db	1	TCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTCACCAAGCTATCCAGAATACAG	60
Qy	883	ATGAAGGCCACCCANTCAGGCATATCTGGAACTCGAAGTTGCTATATCTGAGAGTTGG	942
Db	61	ATGAAGGCCACCCANTCAGGCATATCTGGAACTCGAAGTTGCTATATCTGAGAGTTGG	120
Qy	943	TTCAGAGTACAGTAATCTCTGCTTCGTGCATGTGAACTGCACGATAAAGAACTCAGGC	1002
Db	121	TTCAGAGTACAGTAATCTCTGCTTCGTGCATGTGAACTGCACGATAAAGAACTCAGGC	180
Qy	1003	GCCTCTTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTGATGTGGGTAT	1062
Db	181	GCCTCTTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTGATGTGGGTAT	240
Qy	1063	TTACCTATGTTGGTCCCTGTTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTTAC	1122
Db	241	TTACCTATGTTGGTCCCTGTTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTTAC	300
Qy	1123	TCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCATTTCTAGGAC	1182
Db	301	TCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCATTTCTAGGAC	360
Qy	1183	TTGCAAAATAAGAAATGTTAAAAAGTCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGA	1242
Db	361	TTGCAAAATAAGAAATGTTAAAAAGTCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGA	420
Qy	1243	AGCGAAAGCTGAATGAAAAAGCCCAAAAATAATTAGTAGGAGTTTCATCTTTAAAGGGAT	1302
Db	421	AGCGAAAGCTGAATGAAAAAGCCCAAAAATAATTAGTAGGAGTTTCATCTTTAAAGGGAT	480
Qy	1303	ATTCAATTTGATTTATACGGGGAGGGTTCAGGGAAGAACGAACTTGCAGTTGCAGTGCAGT	1362
Db	481	ATTCAATTTGATTTATACGGGGAGGGTTCAGGGAAGAACGAACTTGCAGTTGCAGTGCAGT	540
Qy	1363	TTCAAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACTGTTGTGAGGAAAAATPACC	1422
Db	541	TTCAAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACTGTTGTGAGGAAAAATPACC	600

Qy	1423	TGCTTTGACTGCCATGTGTTTCATCATCTTAAAGATTATTTGAAGCTGCCTATGTATCGATTTAA	1481
Db	601	TGCTTTGACTGCCATGTGTTTCATCATCTTAAAGATTATTTGAAGCTGCCTATGTATCGATTTAA	660
Qy	1483	ACCGTAATCATATCTTTTTTC-----CTATCTTGAGGCACTGGTGGAAATAAAAAAACCCTGTATA	1538
Db	661	ACCGTAATCATATCTTTTTTCCTTATCTATCTTGAGGCACTGGTGGAAATAAAAAAACCCTGTATA	720
Qy	1539	TTTTTACTTTTGTTCAGATAGTCTTTGCCGCACTCTTGGCAAGCTTCAGAGATGGTGGAGCTA	1598
Db	721	TTTTTACTTTTGTTCAGATAGTCTTTGCCGCACTCTTGGCAGTTGCAGAGATGGTGGAGCTA	780
Qy	1599	GAAAAAIAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGFTCCGTGTAGATTGA	1658
Db	781	GAAAAAIAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGFTCCGTGTAGATTGA	840
Qy	1659	TGCAGATTTTCTCAAAATGAAAATGTTTTTGTGTAGACGAGATCATACCGTGAAGAAGCAGGAATG	1718
Db	841	TGCAGATTTTCTCAAAATGAAAATGTTTTTGTGTAGACGAGATCATACCGTGAAGAAGCAGGAATG	900
Qy	1719	ACAAAGCTTGCTTTTCTGGTATGTTCTTAGTGTGATTTGTGCACTTTTAACTGTATATTAATTAAT	1778
Db	901	ACAAAGCTTGCTTTTCTGGTATGTTCTTAGTGTGATTTGTGCACTTTTAACTGTATATTAATTAAT	960
Qy	1779	GCCAAATATAGTAAATATAGAT	1838
Db	961	GCCAAATATAGTAAATATAGAT	1020
Qy	1839	CTTCCAGCACACCCACAGTGTGTTGATATTTTCAGAGTCAGTCATTGGTTATACATATGTGTAG	1898
Db	1021	CTTCCAGCACACCCACAGTGTGTTGATATTTTCAGAGTCAGTCATTGGTTATACATATGTGTAG	1080
Qy	1899	TTCCAAAGCACATAAGCTAGAAAGAAATATTTCTTAGGAGCACTACCCTCTGTTTCAA	1958
Db	1081	TTCCAAAGCACATAAGCTAGAAAGAAATATTTCTTAGGAGCACTACCCTCTGTTTCAA	1140
Qy	1959	CATGAAATGCCACACACATAGAACTCCAACAACATCAATTTTCAATTGCAAGACTGACTGT	2018
Db	1141	CATGAAATGCCACACACATAGAACTCCAACAACATCAATTTTCAATTGCAAGACTGACTGT	1197
Qy	2019	AGTTAAATTTTGTCCACAGAACTATGCACTGAACTTAATGCTTCCAAAATATGTTGTTGTT	2078
Db	1198	AGTTAAATTTTGTCCACAGAACTATGCACTGAACTTAATGCTTCCAAAATATGTTGTTGTT	1257
Qy	2079	TGCAATATCAAAACATGTTTATGCAAGAAATTTATTAATTTACAAAATGAAGATTTATACCA	2138
Db	1258	TGCAATATCAAAACATGTTTATGCAAGAAATTTATTAATTTACAAAATGAAGATTTATACCA	1317
Qy	2139	TTTGTTTTAAGCTGTACTGAACTTAATCTGTGGAAATGCAATGCTGTGAACTGTAAAGCAA	2198
Db	1318	TTTGTTTTAAGCTGTACTGAACTTAATCTGTGGAAATGCAATGCTGTGAACTGTAAAGCAA	1377
Qy	2199	GTATCAATAAAGCTTATAGACTT 2221	
Db	1378	GTATCAATAAAGCTTATAGACTT 1400	

RESULT 14
US-10-956-157-4532
; Sequence 4532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCI.
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4532


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; LENGTH: 4623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4532

Query Match      61.1%; Score 1369; DB 21; Length 4623;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1466; Conservative 0; Mismatches 0; Indels 67; Gaps 3;

Qy 693 GTTGTGACCTCTCTGACTCGAGAGACATTAAGAAGACTCGAGTGGTGTGGTGCAGC 752
Db 3154 GTTGTGACCTCTCTGACTCGAGAGACATTAAGAAGACTCGAGTGGTGTGGTGCAGC 3213

Qy 753 CTATTCCTGCTGCTTCATTGACAGATATTCAGCATTTGTGACGTAACAGCCTACATGGC 812
Db 3214 CTATTCCTGCTGCTTCATTGACAGATATTCAGCATTTGTGACGTAACAGCCTACATGGC 3273

Qy 813 TTGSCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 872
Db 3274 TTGSCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 3333

Qy 873 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAACTGCTATATCT 932
Db 3334 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAACTGCTATATCT 3393

Qy 933 GAGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTGAACCTGCACGATAAAG 992
Db 3394 GAGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTGAACCTGCACGATAAAG 3453

Qy 993 GAACTCAGGCGCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1052
Db 3454 GAACTCAGGCGCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 3513

Qy 1053 ATGCGGTATTTACTATGTTGGTGCCTTGTGTAATGCTGTGACACTACTGATTTGGCT 1112
Db 3514 ATGCGGTATTTACTATGTTGGTGCCTTGTGTAATGCTGTGACACTACTGATTTGGCT 3573

Qy 1113 CTCATTTCACTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 3574 CTCATTTCACTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 3633

Qy 1173 TATCTAGACTTGCATTAAGATGATTAAGATGCTATGCTAAATCCAAAGCAAAATC 1232
Db 3634 TATCTAGACTTGCATTAAGATGATTAAGATGCTATGCTAAATCCAAAGCAAAATC 3693

Qy 1233 CCTGATTTGAAGCCGCAAGCTGAATGAAACGCCCAAAATTAATAGTAGGATTCATCTT 1292
Db 3694 CCTGATTTGAAGCCGCAAGCTGAATGAAACGCCCAAAATTAATAGTAGGATTCATCTT 3753

Qy 1293 TAAAGGGGATATTCATTTGATTTATACGGGGGAGGGTCAGGGAAGACCAACCTTGACGTT 1352
Db 3754 TAAAGGGGATATTCATTTGATTTATACG----- 3780

Qy 1353 GCAGTGCAATTTACAGATCGTTGTTAGATCTTTATTTTAGCCATGCTGTTGAGG 1412
Db 3781 -----GATCTTTATTTTAGCCATGCTGTTGAGG 3813

Qy 1413 AAAAAATTACCTGCTTGCATGCCATGTTCTCATCATCTTAAGTATTTGAAGCTGCTATGT 1472
Db 3814 AAAAAATTACCTGCTTGCATGCCATGTTCTCATCATCTTAAGTATTTGAAGCTGCTATGT 3873

Qy 1473 ATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCCTGTTGGGAATAAAA 1528
Db 3874 ATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTATCTGAGGCCTGTTGGGAATAAAA 3933

Qy 1529 AACCTGTATATTTTACTTTGTCAGATAGTCTTGGCCGATCTTGGCAAGTTGACAGAT 1588
Db 3934 AACCTGTATATTTTACTTTGTCAGATAGTCTTGGCCGATCTTGGCAAGTTGACAGAT 3993

Qy 1589 GGTGGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTGTATGTCG 1648
Db 3994 GGTGGAGCTAGAAAAAAGCCCTTTTTCAGTTTGTGCACTGTGTATGTCG 4053
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Qy 1649 TGTAGATTGATGCGAGATTTTCTGAAATGAATGTTGTTTGTAGACGAGATCATACCGGTAA 1708
Db 4054 TGTAGATTGATGCGAGATTTTCTGAAATGAATGTTGTTTGTAGACGAGATCATACCGGTAA 4113

Qy 1709 AGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTTAGTGTTATTTGACTTTTACTGT 1768
Db 4114 AGCAGGAATGACAAAGCTTGTCTTTCTGGTATGTTCTTAGTGTTATTTGACTTTTACTGT 4173

Qy 1769 TATATTAAATGCGCAATATAGTAATAATATAGATTATATATATATATATATATATATATAT 1828
Db 4174 TATATTAAATGCGCAATATAGTAATAATATAGATTATATATATATATATATATATATATAT 4233

Qy 1829 AGACCTTTTACCTTCCAGCCACCCACAGTCTTGTGATATTTTCAGAGTCAGTCATTTGGTTAT 1888
Db 4234 AGACCTTTTACCTTCCAGCCACCCACAGTCTTGTGATATTTTCAGAGTCAGTCATTTGGTTAT 4293

Qy 1889 ACATGTGTAGTTCCTCAAGCACAATAAGCTAGCAAGAGAAATATTTCTAGGAGCACTACCAT 1948
Db 4294 ACATGTGTAGTTCCTCAAGCACAATAAGCTAGCAAGAGAAATATTTCTAGGAGCACTACCAT 4353

Qy 1949 CTGTTTTCAACATGAATGCCACACATAGAACTCCAAACAACATCAATTTTCATTGCAACA 2008
Db 4354 CTGTTTTCAACATGAATGCCACACATAGAACTC---CAACATCAATTTTCATTGCAACA 4410

Qy 2009 GACTGACTGTAGTAAATTTTGTACAGAACTCTATGGAATCTAATCTAATGCTTCCAAAAT 2068
Db 4411 GACTGACTGTAGTAAATTTTGTACAGAACTCTATGGAATCTAATCTAATGCTTCCAAAAT 4470

Qy 2069 GTTGTGTTGTTGCAAAATATCAAAATTTTGTATGCAAGAAATTTATTAATTAACAAATGAAG 2128
Db 4471 GTTGTGTTGTTGCAAAATATCAAAATTTTGTATGCAAGAAATTTATTAATTAACAAATGAAG 4530

Qy 2129 ATTTATACCAATTTGGTAAAGCTGTACTGAACTAAATCTGTGAAATGCAATTTGGAATCTG 2188
Db 4531 ATTTATACCAATTTGGTAAAGCTGTACTGAACTAAATCTGTGAAATGCAATTTGGAATCTG 4590

Qy 2189 TAAAGCAAGATATCAATAAGCTTATAGACTT 2221
Db 4591 TAAAGCAAGATATCAATAAGCTTATAGACTT 4623

RESULT 15
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-62

Query Match      60.7%; Score 1359.2; DB 17; Length 1785;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 8; Indels 5; Gaps 4;

Qy 692 GGTGTGTGACCTCTCTGACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 751
Db 246 GGTGTGTGACCTCTCTGACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 305

Qy 752 CCTATTCTCTGCTCTTTCATTGACGATTTTCAGCATTTGTCAGCGTACACGCTACATTGC 811
Db 306 CCTATTCTCTGCTCTTTCATTGACGATTTTCAGCATTTGTCAGCGTACACGCTACATTGC 365
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Qy	812	CTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT	871
Db			
Qy	366	CTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT	425
Db			
Qy	872	CCAGAAATCAGATGAAGCCCAACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC	931
Db			
Qy	426	CCAGAAATCAGATGAAGCCCAACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC	485
Db			
Qy	932	TGAGGAGTTGGTTGAGAGTACAGTAATCTGCTCTTGGTCTGATGTGAATCTGACGATGATAA	991
Db			
Qy	486	TGAGGAGTTGGTTGAGAGTACAGTAATCTGCTCTTGGTCTGATGTGAATCTGACGATGATAA	545
Db			
Qy	992	GGAACTCAGGGCGCTCTCTTCTAGTTGATGATTAAGTTAGTTGATCTCTGAAAGTTTGCAAGTGT	1051
Db			
Qy	546	GGAACTCAGGGCGCTCTCTTCTAGTTGATGATTAAGTTAGTTGATCTCTGAAAGTTTGCAAGTGT	605
Db			
Qy	1052	GATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGGTCTGACATCTGATGATTTGGC	1111
Db			
Qy	606	GATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGGTCTGACATCTGATGATTTGGC	665
Db			
Qy	1112	TCTCATTTTCATCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCA	1171
Db			
Qy	666	TCTCATTTTCATCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCA	725
Db			
Qy	1172	TTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAAT	1231
Db			
Qy	726	TTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAAT	785
Db			
Qy	1232	CCCTGGATTTGAAGCGCAAGCTGAATGAATAACGGCCAAAATAATTTAGTAGGAGTTTCATCT	1291
Db			
Qy	786	CCCTGGATTTGAAGCGCAAGCTGAATGAATAACGGCCAAAATAATTTAGTAGGAGTTTCATCT	845
Db			
Qy	1292	TTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAGAAACGAACCTTTGAGCT	1351
Db			
Qy	846	TTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAGAAACGAACCTTTGAGCT	905
Db			
Qy	1352	TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACCTGTTGTGAG	1411
Db			
Qy	906	TGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACCTGTTGTGAG	965
Db			
Qy	1412	GAAAAATTAACCTGCTTGACCTGCCATGTGTTCACTTAAGTATTTGTAAGCTGCTATG	1471
Db			
Qy	966	GAAAAATTAACCTGCTTGACCTGCCATGTGTTCACTTAAGTATTTGTAAGCTGCTATG	1025
Db			
Qy	1472	TATGATTTTAAACCGTATCATATCTTTTCTATCTGAGGCACTGGTGGATAAAAAC	1531
Db			
Qy	1026	TATGATTTTAAACCGTATCATATCTTTTCTATCTGAGGCACTGGTGGATAAAAAC	1085
Db			
Qy	1532	CTGTATATTTTACTTTTGTGAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGT	1591
Db			
Qy	1086	CTGTATATTTTACTTTTGTGAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGT	1145
Db			
Qy	1592	GGAGCTAG-AAAAAATAAGGAGGCTTTTCAAGTTTGTGCACTGTGTATGTTCCGCTG	1650
Db			
Qy	1146	GGAGCTAGAAAAAATAAGGAGGCTTTTCAAGTTTGTGCACTGTGTATGTTCCGCTG	1205
Db			
Qy	1651	TAGATTTGATGAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAG	1710
Db			
Qy	1206	TAGATTTGATGAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAG	1265
Db			
Qy	1711	CAGGAATGACAAAGCTTCTGTTTCTGGTATGTTCTAGGTATTTGTGATCTTTTACTGTTA	1770
Db			
Qy	1266	CAGGAATGACAAAGCTTCTGTTTCTGGTATGTTCTAGGTATTTGTGATCTTTTACTGTTA	1325
Db			
Qy	1771	TATTAAATGCCAATAAAGTAAATATAGATTATATATATAGTGTTCACAAAGCTTTAG	1830
Db			
Qy	1326	TATTAAATGCCAATAAAGTAAATATAGATTATATATATAGTGTTCACAAAGCTTTAG	1385
Db			
Qy	1831	ACCTTTTACCTTCCAGCCACCCACAGTCTGTGATATTTTACAGTCTGATTTGGTTATAC	1890
Db			
Qy	1386	ACCTTTTACCTTCCAGCCACCCACAGTCTGTGATATTTTACAGTCTGATTTGGTTATAC	1445
Db			

Qy	1891	ATGTGTAGTTCCAAAGCACATAAGCTAGAGAGAGAAATATTTCTAGGAGCACTACCATCT	1950
Db			
Qy	1446	ATGTGTAGTTCCAAAGCACATAAGCTAGAGAGAGAAATATTTCTAGGAGCACTACCATCT	1505
Db			
Qy	1951	GTTTTCAACATGAATGCCACACACATAGAACTCCAAACACATCAATTTCAATTCACACAGA	2010
Db			
Qy	1506	GTTTTCAACATGAATGCCACACACATAGAACTCCAAACACATCAATTTCAATTCACACAGA	1565
Db			
Qy	2011	CTGACTGTAGTTAATTTTGTCCACAGAAATCTATGGAATCTAATCTAATGCTTCCAAAAATGT	2070
Db			
Qy	1566	CTGACTGTAGTTAATTTTGTCCACAGAAATCTATGGAATCTAATGCTTCCAAAAATGT	1623
Db			
Qy	2071	TGTTTGTGCAAAATATCAAAACATTTGTTATGCAAGAAATTAAT	2112
Db			
Qy	1624	TGTTTGTGTT--GCAAAATACCAACATTTGTTATGCCAGAAATTTT	1663
Db			

Search completed: August 1, 2005, 20:25:49
Job time : 1318 secs

Record No.	Score	Match	Length	ID	Description
1	1525.2	68.1	4822	3	US-09-484-9708-106
2	1405	62.7	1669	4	US-09-949-016-3253
3	1097.6	49.0	2810	4	US-09-023-655-382
4	996.2	44.5	42075	4	US-09-949-016-14995
5	682	30.4	799	2	US-08-700-607-2
6	521	23.3	536	4	US-09-621-976-3839
7	514	22.9	537	4	US-09-513-999C-10680
8	482	21.5	508	4	US-09-621-976-3840
9	381.8	17.0	496	4	US-09-513-999C-11204
10	343	15.3	441	4	US-09-513-999C-2227
11	316.6	14.1	463	4	US-09-621-976-741
12	316	14.1	454	4	US-09-621-976-740
13	270.4	12.1	2069	4	US-09-949-016-3309
14	270.4	12.1	3202	4	US-09-949-016-1127
15	263	11.7	301	3	US-09-439-313-279
16	263	11.7	301	3	US-09-352-618A-279
17	263	11.7	301	3	US-09-232-149A-279
18	263	11.7	301	4	US-09-159-813-279
19	263	11.7	301	4	US-09-636-215-279
20	263	11.7	301	4	US-09-685-168A-279
21	263	11.7	301	4	US-09-688-489-279
22	263	11.7	301	4	US-09-679-426-279
23	263	11.7	301	4	US-09-759-143-279
24	263	11.7	301	4	US-09-651-236-279
25	244.8	10.9	1766	3	US-09-149-476-254
26	244.8	10.9	2664	3	US-09-149-476-255
27	236.4	10.6	2662	4	US-09-949-016-2988

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QY 993 GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 1052
Db 3568 GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 3627
QY 1053 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGCTGTCACACTACTGATTTGGCT 1112
Db 3628 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGCTGTCACACTACTGATTTGGCT 3687
QY 1113 CTCAATTTCACTCTTTCAGTGTGTTCTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 3688 CTCAATTTCACTCTTTCAGTGTGTTCTTATTTATGAACGGCATCAGGCACAGATAGATCAT 3747
QY 1173 TATCTAGACTTGCATAAAGATGTTAAAGATGCTATGGCTTAAATCAAAATCAAGCAAAAATC 1232
Db 3748 TATCTAGACTTGCATAAAGATGTTAAAGATGCTATGGCTTAAATCAAAATCAAGCAAAAATC 3807
QY 1233 CTGTGATTTGACGCGCAAGCTGAATGAAGAACGCCCAAAATTAATAGTAGGAGTTTCATCTT 1292
Db 3808 CTGTGATTTGACGCGCAAGCTGAATGAAGAACGCCCAAAATTAATAGTAGGAGTTTCATCTT 3867
QY 1293 TAAAGGGATATTTCAATTTGATTTATACGGGGAGGCTCAGGGAAGAACGAACTTGACGTT 1352
Db 3868 TAAAGGGATATTTCAATTTGATTTATACGGGGAGGCTCAGGGAAGAACGAACTTGACGTT 3927
QY 1353 GCAGTGCAGTTTTCAGATCGTTGTTAGATCTTTATTTTATAGCCATGCACTGTTGTGAGG 1412
Db 3928 GCAGTGCAGTTTTCAGATCGTTGTTAGATCTTTATTTTATAGCCATGCACTGTTGTGAGG 3987
QY 1413 AAAAATTAACCTGCTTTGACTGCCATGTTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 1472
Db 3988 AAAAATTAACCTGCTTTGACTGCCATGTTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 4047
QY 1473 ATGGATTTTAAACCGTAATCATATCTTTTCTTATCTGAGGCACCTGGTGGAAATAAAAACC 1532
Db 4048 ATGGATTTTAAACCGTAATCATATCTTTTCTTATCTGAGGCACCTGGTGGAAATAAAAACC 4107
QY 1533 TGTATATTTATTTTGTGTCAGATAGTCTTGCCGCATCTTGCCAGTTTGCAGAGATGGT 1592
Db 4108 TGTATATTTATTTTGTGTCAGATAGTCTTGCCGCATCTTGCCAGTTTGCAGAGATGGT 4167
QY 1593 GAGCTAG--AAAAAATAAAGCCCTTTTTCAGTTTGTGCACTGTTGTTGCTCGTG 1650
Db 4168 GAGCTAGAAAAAATAAAGCCCTTTTTCAGTTTGTGCACTGTTGTTGCTCGTG 4227
QY 1651 TAGATTGATGCAATTTTCTGAAATGAAATGTTGTTTGTAGACGAGATCATACCGGTAAG 1710
Db 4228 TAGATTGATGCAATTTTCTGAAATGAAATGTTGTTTGTAGACGAGATCATACCGGTAAG 4287
QY 1711 CAGGAATGCAAAAGCTTCTTTTCTGATGTTTCTAGGTGATTTGTTGATCTTTTACTGTTA 1770
Db 4288 CAGGAATGCAAAAGCTTCTTTTCTGATGTTTCTAGGTGATTTGTTGATCTTTTACTGTTA 4347
QY 1771 TATTAATTTGCCATATATAGTAAATATAGATTTATATATATGTTGTTTTCACAAAGCTTAG 1830
Db 4348 TATTAATTTGCCATATATAGTAAATATAGATTTATATATATGTTGTTTTCACAAAGCTTAG 4407
QY 1831 ACCTTTACCTTCCAGCCACCCACAGTCTTGATATTTTTCAGAGTCAGTCATTGGTTATAC 1890
Db 4408 ACCTTTACCTTCCAGCCACCCACAGTCTTGATATTTTTCAGAGTCAGTCATTGGTTATAC 4467
QY 1891 ATGTGTAGTTCCAAAGCACAATAGCTAGAAGAAATATTTTCTAGGAGCACTACCAATCT 1950
Db 4468 ATGTGTAGTTCCAAAGCACAATAGCTAGAAGAAATATTTTCTAGGAGCACTACCAATCT 4527
QY 1951 GTTTTCAACATGAATGCGACACATAGAACTCCAAACATCAATTTCAATTGACACAGA 2010
Db 4528 GTTTTCAACATGAATGCGACACATAGAACTCCAAACATCAATTTCAATTGACACAGA 4587
QY 2011 CTGACTGTAGTTTAAATTTTGTACAGAACTTATGGAATCTAATGCTTCCAAAAATGT 2070
Db 4588 CTGACTGTAGTTTAAATTTTGTACAGAACTTATGGAATCTAATGCTTCCAAAAATGT 4647
QY 2071 TGTTTGTTTGCATAATCAAAATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAGAT 2130
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Db 4648 TGTTTGTTTGCATAATCAAAATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAGAT 4707
QY 2131 TTATACCAATTTGCTGTTTAAAGCTGACTGAACATAATCTGTGGAATGCAATCTGAACTGTA 2190
Db 4708 TTATACCAATTTGCTGTTTAAAGCTGACTGAACATAATCTGTGGAATGCAATCTGAACTGTA 4767
QY 2191 AAAGCAAAAGTATCAATAAAGCTTATAGACTTTAAAAAATAAATAAATAAATAAATAA 2240
Db 4768 AAAGCAAAAGTATCAATAAAGCTTATAGACTTTAAAAAATAAATAAATAAATAAATAA 4817
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RESULT 2

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US-09-949-016-3253
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3253
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3253
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Query Match 62.7%; Score 1405; DB 4; Length 1669;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1419; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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QY 692 GGTGTTGACCTCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTGTTGTCGAC 751
Db 247 GGTGTTGACCTCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTGTTGTCGAC 306
QY 752 CCTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATTTGAGCGCTAACAGCCTACATTGC 811
Db 307 CCTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATTTGAGCGCTAACAGCCTACATTGC 366
QY 812 CTGCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTAT 871
Db 367 CTGCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTAT 426
QY 872 CCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 931
Db 427 CCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 486
QY 932 TGAGGAGTTGGTTCCAGAAAGTACAGTAATCTGCTCTTGGTTCATGTAACCTGACGATAAA 991
Db 487 TGAGGAGTTGGTTCCAGAAAGTACAGTAATCTGCTCTTGGTTCATGTAACCTGACGATAAA 546
QY 992 GGAATCAGGCGCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGT 1051
Db 547 GGAATCAGGCGCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGT 606
QY 1052 GATGTGGGTATTTACCTATGTTGTCCTTGTGTTAAATGCTGACACTACTGATTTTGGC 1111
Db 607 GATGTGGGTATTTACCTATGTTGTCCTTGTGTTAAATGCTGACACTACTGATTTTGGC 666
QY 1112 TCTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1171
Db 667 TCTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 726
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QY 1172 TTATCTAGGACTTCAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 1231
Db 727 TTATCTAGGACTTCAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 786
QY 1232 CCCTGGATTTGAAGCGCAAGCTGAATGAAACGCCCAAAATAAATTAGTAGGAGTTCACT 1291
Db 787 CCCTGGATTTGAAGCGCAAGCTGAATGAAACGCCCAAAATAAATTAGTAGGAGTTCACT 846
QY 1292 TTAAGGGGATATTCATTTGATTTATACGGGGGAGGTCAGGGAAGAACGAACCTTGACGT 1351
Db 847 TTAAGGGGATATTCATTTGATTTATACGGGGGAGGTCAGGGAAGAACGAACCTTGACGT 906
QY 1352 TGCACTGCAAGTTTCAAGATGCTTTAGATCTTTATTTTATAGCCATGCTGTTGAG 1411
Db 907 TGCACTGCAAGTTTCAAGATGCTTTAGATCTTTATTTTATAGCCATGCTGTTGAG 966
QY 1412 GAAAAATTTACCTGCTTTCAGCTGCCATGTTTCATCATCTTAAGTATTTAGCTGCTATG 1471
Db 967 GAAAAATTTACCTGCTTTCAGCTGCCATGTTTCATCATCTTAAGTATTTAGCTGCTATG 1026
QY 1472 TATGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACTGGTGAATAAA 1527
Db 1027 TATGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGGTGAATAAA 1086
QY 1528 AAACCTGTATATTTTACCTTTTTCAGATAGTCTTTCGCGCATCTTGCAGAGTTGCAGAGA 1587
Db 1087 AAACCTGTATATTTTACCTTTTTCAGATAGTCTTTCGCGCATCTTGCAGAGTTGCAGAGA 1146
QY 1588 TGGTGGAGCTAGAAAAAAGGCAAGGCTTTTTCAGTTTGTGCTGCTGTTGATGCTCC 1647
Db 1147 TGGTGGAGCTAGAAAAAAGGCAAGGCTTTTTCAGTTTGTGCTGCTGTTGATGCTCC 1206
QY 1648 GTGTAGATTGATGAGATTTTTCGAAATGAAATGTTTGTGAGCAGATCATACCGGTA 1707
Db 1207 GTGTAGATTGATGAGATTTTTCGAAATGAAATGTTTGTGAGCAGATCATACCGGTA 1266
QY 1708 AAGCAGAAATGACAAAGCTTCTTTCGATGATGTTTCTAGTGTATTTGAGCTTTTACTG 1767
Db 1267 AAGCAGAAATGACAAAGCTTCTTTCGATGATGTTTCTAGTGTATTTGAGCTTTTACTG 1326
QY 1768 TTATTAATTTGCCAATATAGTAAATATAGATTATATATAGTATGTTTTCACAAAGCT 1827
Db 1327 TTATTAATTTGCCAATATAGTAAATATAGATTATATATAGTATGTTTTCACAAAGCT 1386
QY 1828 TAGACCTTTTACCTTCCAGCCACCCACAGCTGCTTGTATTTTCAGAGTCAGTCATTGGTTA 1887
Db 1387 TAGACCTTTTACCTTCCAGCCACCCACAGCTGCTTGTATTTTCAGAGTCAGTCATTGGTTA 1446
QY 1888 TACATGTGTAGTTCCAAAGCACAATAAGCTAGAGAAGAAATATTTTCAGAGGCACTACCA 1947
Db 1447 TACATGTGTAGTTCCAAAGCACAATAAGCTAGAGAAGAAATATTTTCAGAGGCACTACCA 1506
QY 1948 TCTGTTTTCACATGAATGCCACACATAGAACTCCAAACATCAATCAATTTCAATTCGCAC 2007
Db 1507 TCTGTTTTCACATGAATGCCACACATAGAACTCCAAACATCAATCAATTTCAATTCGCAC 1566
QY 2008 AGACTGACTGTAGTTAAATTTTGTTCACAGAACTTATGGAATCTAATGCTTCCAAAAA 2067
Db 1567 AGACTGACTGTAGTTAAATTTTGTTCACAGAACTTATGGAATCTAATGCTTCCAAAAA 1626
QY 2068 TGTGTTTGTTCAAATATCAAAATTTGATGCAAGAAAT 2110
Db 1627 TGTGTTTGTTCAAATATCAAAATTTGATGCAAGAAAT 1669

RESULT 3

US-09-023-655-382
; Sequence 382, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONS: 1508778
; US-09-023-655-382

Query Match 49.0%; Score 1097.6; DB 4; Length 2610;
Best Local Similarity 98.4%; Pred. No. 2.6e-255;
Matches 1172; Conservative 0; Mismatches 10; Indels 9; Gaps 6;
QY 692 GGTGTTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 751
Db 1310 GGTGTTTGACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 1369
QY 752 CCTATTCTGCTGCTCTTTCATTTGACAGTATTCAGCATTTGAGCGGTAAACAGCTAC-ATTG 810
Db 1370 CCTATTCTGCTGCTCTTTCATTTGACAGTATTCAGCATTTGAGCGGTAAACAGCTACAAATTG 1429
QY 811 CCTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAGGGTGTGATCCAACTA 870
Db 1430 CCTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAGGGTGTGATCCAACTA 1489
QY 871 TCCAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGAAGTTGCTATAT 930
Db 1490 TCCAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGAAGTTGCTATAT 1549
QY 931 CTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTCTCTTGGTCAATGTGAACCTGACGATAA 990
Db 1550 CTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTCTCTTGGTCAATGTGAACCTGACGATAA 1609
QY 991 AGGAATCTAGGCGCTCTCTTCTAGTATGATTTAGTATTTCTGAACTTTCAGTGT 1050
Db 1610 AGGAATCTAGGCGCTCTCTTCTAGTATGATTTAGTATTTCTGAACTTTCAGTGT 1669
QY 1051 TGATGTGGGTATTTTACCTATGTTGGCTCTGTTTAAATGCTGACACTACTGATTTGG 1110
Db 1670 TGATGTGGGTATTTTACCTATGTTGGCTCTGTTTAAATGCTGACACTACTGATTTGG 1729

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QY 1111 CTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 1170
Db 1730 CTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 1789
QY 1171 ATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAAA 1230
Db 1790 ATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAAA 1849
QY 1231 TCCCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGAGTTCAATC 1290
Db 1850 TCCCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATAATTAGTAGGAGTTCAATC 1909
QY 1291 TTTAAAGGGGATATTCATTTGA- TTATACGGGGAGGGTCAAGGGAAGAACCAACCTTGAC 1349
Db 1910 TTTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAAGGGAAGAACCAACCTTGAC 1969
QY 1350 GTTGCAGTGCAGTTTTCAGATCGGTGTTAGATCTTTTATTTTACGCCATGCACCTGTTGTG 1409
Db 1970 GTTGCAGTGCAGTTTTCAGATCGGTGTTAGATCTTTTATTTTATAGCCATGCACCTGTTGTG 2029
QY 1410 AGGAAAAATTACCTGCTTTGACTGCGCATGTTTCATCATCTTAAGTATTTGAAGCTGCTA 1469
Db 2030 AGGAAAAATTACCTGCTTTGACTGCGCATGTTTCATCATCTTAAGTATTTGAAGCTGCTA 2089
QY 1470 TGTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGGTGAATA 1525
Db 2090 TGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGAATA 2149
QY 1526 AAAACCTGTATATTTTACTTTGTTGACATAGTCTTCCGCATCTTGGCAAGTGCAGA 1585
Db 2150 AAAACCTGTATATTTTACTTTGTTGACATAGTCTTCCGCATCTTGGCAAGTGCAGA 2209
QY 1586 GATGTGTGAGCTAGAAAAA-----AAAAAAGCCCTTTTCAGTTTGTGCACCTGTGTATGG 1644
Db 2210 GATGTGTGAGCTAGAAAAA-----AAAAAAGAGCCCTTTTCAGTTTGTGCACCTGTGTATGG 2269
QY 1645 TCCGTGTAGATGATGACAGATTTCTGAAAAGAAATGTTGTTAGACAGATCATA-CC 1703
Db 2270 TCCGTGTAGATGATGACAGATTTCTGAAAAGAAATGTTGTTAGACAGATCATAACC 2329
QY 1704 GGTAAAGCAGGAATCAGAAAGCTTTCTTCTGTTATGCTTCTAGGTGATTTGTGACTTTT 1763
Db 2330 GGTAAAGCAGGAATCAGAAAGCTTTCTTCTGTTATGCTTCTAGGTGATTTGTGACTTTT 2389
QY 1764 ACTGTTATATTAATTTGCCAATAATAGTAAATATAGATTTATATATATAGTGTTCACAA 1823
Db 2390 ACTGTTATATTAATTTGCCAATAATAGTAAATATAGATTTATATATATAGTGTTCACAA 2449
QY 1824 AGCTTA-GACCTTTACCTTCCAGCCACCCACAGCTGTGATTTTCAGAG 1873
Db 2450 AGCTTAGGACCTTTACCTTCCAGCCACCCACAGCTGTGATTTTCAGAG 2500
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RESULT 4

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US-09-949-016-14995
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
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; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995

Query Match 44.5%; Score 996.2; DB 4; Length 42075;
Best Local Similarity 97.9%; Pred. No. 5e-230;
Matches 1021; Conservative 0; Mismatches 18; Indels 4; Gaps 1;

QY 1189 ATAAGAAATGTTAAAGATGCTATGCTAAATCAAGCAAAATCCCTGGATTGAAGCGCA 1248
Db 39149 ATATTTACATTTGACTTTTCATTTTCAGATCCAGCAAAATCCCTGGATTGAAGCGCA 39208
QY 1249 AAGCTGAATGAAAAAGCGCCAAATAATTAGTAGGAGTTCAATCTTTAAAGGGGATATTCAT 1308
Db 39209 AAGCTGAATGAAAAAGCGCCAAATAATTAGTAGGAGTTCAATCTTTAAAGGGGATATTCAT 39268
QY 1309 TTGATTATACGGGGAGGGTCAGGGAAGAACCAACCTTGACGTTGCAAGTGCAGTTTCA 1368
Db 39269 TTGATTATACGGGGAGGGTCAGGGAAGAACCAACCTTGACGTTGCAAGTGCAGTTTCA 39328
QY 1369 GATCGTTGTTAGATCTTTTATTTTAGCCATCAGCTGTTGTGAGGAAAAATTTACCTGTCTT 1428
Db 39329 GATCGTTGTTAGATCTTTTATTTTAGCCATGCACTGTTGTGAGGAAAAATTTACCTGTCTT 39388
QY 1429 GACTGCCATGTGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATTTAAACCGTA 1488
Db 39389 GACTGCCATGTGTTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATGATTTAAACCGTA 39448
QY 1489 ATCATATCTTTTTC-----CTATCTGAGGCACCTGTGGAATAAAAAACCTGTATATTTTAC 1544
Db 39449 ATCATATCTTTTTCCTATCTATCTGAGGCACCTGTGGAATAAAAAACCTGTATATTTTAC 39508
QY 1545 TTTGTTGACAGATGCTTTGCGCATCTTGGCAAGTTGACAGATGTTGAGGAGTGAAGAAAA 1604
Db 39509 TTTGTTGACAGATGCTTTGCGCATCTTGGCAAGTTGACAGATGTTGAGGAGTGAAGAAAA 39568
QY 1605 AAAAAAAGCCCTTTTCAGTTTGTGCACCTGTGTATGTTGCTGCTAGATGATGACAGA 1664
Db 39569 AAAAAAAGCCCTTTTCAGTTTGTGCACCTGTGTATGTTGCTGCTAGATGATGACAGA 39628
QY 1665 TTTTCTGAAATGAAATGTTTGTGTTAGACAGATCATACCGTAAAGCAGGATGACAAAG 1724
Db 39629 TTTTCTGAAATGAAATGTTTGTGTTAGACAGATCATACCGTAAAGCAGGATGACAAAG 39688
QY 1725 CTTCCTTTCTGCTATGTTCTAGGTGATTTGCTGACTTTTACTGTTATATTAATTAATTTGCCAAT 1784
Db 39689 CTTCCTTTCTGCTATGTTCTAGGTGATTTGCTGACTTTTACTGTTATATTAATTAATTTGCCAAT 39748
QY 1785 ATAAGTAAATATAGATTTATATATATATAGTGTGTTTACAAAAGCTTAGACCTTTTACCTTCCA 1844
Db 39749 ATAAGTAAATATAGATTTATATATATATAGTGTGTTTACAAAAGCTTAGACCTTTTACCTTCCA 39808
QY 1845 GCCACCCACAGCTGCTGATTTATTTTTCAGATGCTATGTTTATACATGTTAGTTTCCAA 1904
Db 39809 GCCACCCACAGCTGCTGATTTATTTTTCAGATGCTATGTTTATACATGTTAGTTTCCAA 39868
QY 1905 AGCATAAGCTAGCAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCACATGAA 1964
Db 39869 AGCATAAGCTAGCAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCACATGAA 39928
QY 1965 ATGCCACACATAGAACTCCAAACAACATCAATTTTCATTGACAGACTGCTGTAGTTAA 2024
Db 39929 ATGCCACACATAGAACTCCAAACAACATCAATTTTCATTGACAGACTGCTGTAGTTAA 39988
QY 2025 TTTTGTACAGAAATCTATGAGCTGAATCTAATGCTTCCAAAAATGTTGTTTGGAAA 2084
Db 39989 TTTTGTACAGAAATCTATGGAATCTAATGCTTCCAAAAATGTTGTTTGGAAA 40048
QY 2085 TATCAAAACATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAGATTTATACCAATTTGG 2144
Db 40049 TATCAAAACATTTGTTATGCAAGAAATTTATTAATTAACAAATGAAGATTTATACCAATTTGG 40108
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QY 2145 TTTAAGCTGTACTGAACCTAATCTGTGAATGCACTGTGAACCTGAACCAAGATATCA 2204
Db 40109 TTTAAGCTGTACTGAACCTAATCTGTGAATGCACTGTGAACCTGAACCAAGATATCA 40168
QY 2205 ATAAAGCTTATAGACTTAAAAA 2227
Db 40169 ATAAAGCTTATAGACTTAAAAA 40191

RESULT 5

US-08-700-607-2
; Sequence 2, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus

US-08-700-607-2

Query Match 30.4%; Score 682; DB 2; Length 799;
Best Local Similarity 99.9%; Pred. No. 5.4e-155;
Matches 693; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 692 GGTGTTGACCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 751
Db 107 GGTGTTGACCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAG 166
QY 752 CCTATTCTGCTGCTTTTCATTGACAGATTTTCAGCATTTGAGCGCTAACAGCCTACATTGC 811
Db 167 CCTATTCTGCTGCTTTTCATTGACAGATTTTCAGCATTTGAGCGCTAACAGCCTACATTGC 226
QY 812 CTGCGCCCTGCTCTCTGTCGACATCAGCTTTAGATATACAAAGGCTGATCCAGCTAT 871
Db 227 CTGCGCCCTGCTCTCTGTCGACATCAGCTTTAGATATACAAAGGCTGATCCAGCTAT 286
QY 872 CCAGAAATCAGATGAAGCCACCCATTCAGGGCATCTCGGAATCTGAAGTTGCTATATC 931
Db 287 CCAGAAATCAGATGAAGCCACCCATTCAGGGCATCTCGGAATCTGAAGTTGCTATATC 346

QY 932 TGAGGAGTTGGTTTCAGAACTACAGTAATCTCTGCTCTTGGTTCATGTGAACCTGCACGATAAA 991
Db 347 TGAGGAGTTGGTTTCAGAACTACAGTAATCTCTGCTCTTGGTTCATGTGAACCTGCACGATAAA 406
QY 992 GGAACCTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1051
Db 407 GGAACCTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 466
QY 1052 GATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAAATGGTCTGACACTACTGATTTTGGC 1111
Db 467 GATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAAATGGTCTGACACTACTGATTTTGGC 526
QY 1112 TCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGCATCAGGCACAGATAGATCA 1171
Db 527 TCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGCATCAGGCACAGATAGATCA 586
QY 1172 TTATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAT 1231
Db 587 TTATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAT 646
QY 1232 CCTGGATTGAAGCGCAAAAGCTGAATGAAGAAACGCCCAAAATAATTAGTAGGAGTTCACT 1291
Db 647 CCTGGATTGAAGCGCAAAAGCTGAATGAAGAAACGCCCAAAATAATTAGTAGGAGTTCACT 706
QY 1292 TTAAAGGGGATATTCATTGATTTATACGGGGGAGGTCAGGGAAGAACCTTGAGCT 1351
Db 707 TTAAAGGGGATATTCATTGATTTATACGGGGGAGGTCAGGGAAGAACCTTGAGCT 765
QY 1352 TGCAGTGCAGTTTTCACAGATCGTTGTTAGATCTT 1385
Db 766 TGCAGTGCAGTTTTCACAGATCGTTGTTAGATCTT 799

RESULT 6

US-09-621-976-3839
; Sequence 3839, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3839
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..224
; US-09-621-976-3839

Query Match 23.3%; Score 521; DB 4; Length 536;
Best Local Similarity 99.4%; Pred. No. 4.1e-116;
Matches 534; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1672 AAATGAATGTTTGTGTTAGACGATCATACCGGTAAAGCAGGAATGCAAAAGCTTGCTT 1731
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Db 61 TTCTGGTATGTTCTTAGTGTGTTTGTGACTTTTACTGTTATATTAATGCGCAATATAGTA 120
QY 1792 AATATAGATTATATATGTATAGTGTGTTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCC 1851
Db 121 AATATAGATTATATATGTATAGTGTGTTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCC 180

1335
692
693

Db 301 ACACATAGAACTC---CAACATCAATTTTCATTGACAGACTGACTGTAGTTAATTTTGTC 357
Qy 2032 ACAGATCTATGACTGAATCAATTAAGTTCACAAAATGTTGTTTGGTTTGCATAATATCAAA 2091
Db 358 ACAGATCTATGACTGAATCAATTAAGTTCACAAAATGTTGTTTGGTTTGCATAATATCAAA 417
Qy 2092 CATTTGTTATGCAAGAAATTTAATTAACAAATCAAGATTATACCAATTTGTTTGAAGC 2151
Db 418 CATTTGTTATGCAAGAAATTTAATTAACAAATCAAGATTATACCAATTTGTTTGAAGC 477
Qy 2152 TGTACTGAATCAATCTG 2169
Db 478 TGTACTGAATCAATCTG 495
RESULT 9
US-09-513-999C-11204
; Sequence 11204, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11204
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 486
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-11204
Query Match 17.0%; Score 381.8; DB 4; Length 496;
Best Local Similarity 95.5%; Pred. No. 2e-82;
Matches 403; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
Qy 1189 ATAGAAATGTTAAGATGCTATGCTAAATCCCAAGCAAAATCCCTGGATTGAAGCGCA 1248
Db 76 ATATTTCAATGACTTTTTCATTTTTCAGAAATCCCAAGCAAAAT-CCTGGATTGAAGCGCA 134
Qy 1249 AAGCTGAATGAAACGCGCCAAATAATTTAGTAGAGTTTCATCTTTAAAGGGGATATTCAT 1308
Db 135 AAGCTGAATGAAACGCGCCAAATAATTTAGTAGAGTTTCATCTTTAAAGGGGATATTCAT 194
Qy 1309 TTGAATATACGGGGAGGTCAGGGAAGAACCACTTGAAGTTGCAAGTCAGTCAGTTTCA 1368
Db 195 TTGAATATACGGGGAGGTCAGGGAAGAACCACTTGAAGTTGCAAGTCAGTTTCA 254
Qy 1369 GATCGTTGTTAGATCTTTATTTTATAGCATGCTGTTGTTGAGGAAATTAACCTGCTTT 1428
Db 255 GATCGTTGTTAGATCTTTATTTTATAGCATGCTGTTGTTGAGGAAATTAACCTGCTTT 314
Qy 1429 GACTGCCATGTTTCATCATCTTAAGTATTTAGTGTCTATGATGATTAACCGTA 1488
Db 315 GACTGCCATGTTTCATCATCTTAAGTATTTAGTGTCTATGATGATTAACCGTA 374
Qy 1489 ATCATATCTTTTCTATCTAGGACCTGGTGGGAATAAAAAACCTGTATATTTTACTTTG 1548
Db 375 ATCATATCTTTTCTATCTAGGACCTGGTGGGAATAAAAAACCTGTATATTTTACTTTG 434
Qy 1549 TTGAGATAGCTTTGCCGATCTTTGGCAAGTTTGCAGAGATGTTGCAGATAGTAAAGAAAA 1608
Db 435 TTGAGATAGCTTTGCCGATCTTTGGCAAGTTTGCAGAGATGTTGCAGATAGTAAAGAAAA 494

Qy 1609 AA 1610
Db 495 AA 496

RESULT 10

US-09-513-999C-2227
; Sequence 2227, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2227
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 236..439
US-09-513-999C-2227

Query Match 15.3%; Score 343; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCACACAGTAGTATGCTTCGGCTCAGTCGGGCCAGCCCCCTCTCAGTCTCTCCCAACCC 60
Db 99 CGTCACACAGTAGTATGCTTCGGCTCAGTCGGGCCAGCCCCCTCTCAGTCTCTCCCAACCC 158
Qy 61 CCACACCGCCCGGCTCTGAGACGGCGCCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 159 CCACACCGCCCGGCTCTGAGACGGCGCCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 218
Qy 121 ATCTCCACCTCCAGCCATGGAAGACCTGACCAAGTCTCTCTGCTCTCTCTCTCTCTCTCTCT 180
Db 219 ATCTCCACCTCCAGCCATGGAAGACCTGACCAAGTCTCTCTGCTCTCTCTCTCTCTCTCTCT 278
Qy 181 GCCACCCCGCGCGAGCCCGCTTCAAGTACCAAGTTCGTTGAGGAGCCCGGAGGACGAGG 240
Db 279 GCCACCCCGCGCGAGCCCGCTTCAAGTACCAAGTTCGTTGAGGAGCCCGGAGGACGAGG 338
Qy 241 AGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 339 AGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 398
Qy 301 TGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 343
Db 399 TGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 441

RESULT 11

US-09-621-976-741
; Sequence 741, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21


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Db 934 CAGAAACCGAGAGGCCACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCTTTCT 993
Qy 933 GAGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTCAATGAACTGCACGATAAAG 992
Db 994 CAGGAGCAGATTCAGAAAGTACACGAGCTCCCTGCGAGTTCTACGTGAACAGCACACTTAAG 1053
Qy 993 GAACCTCAGGCGCCTCTTCTTGTGATGATGATTTAGTTGATTTCTCTGAGTTTGCAGTGTG 1052
Db 1054 GAACCTGAGGAGGCTCTTCTTGTGTCAGGACCTGTGTGATTCCTTAAATTTGCAGTCTG 1113
Qy 1053 ATGTGGGTATTTACTATGTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTTGGCT 1112
Db 1114 ATGTGGCTCTGACCTAGTTGGGCTCTCTTCAATGGCTGACCTGCTCTCATGGCT 1173
Qy 1113 CTCAATTCACCTCTTCAGTGTTCCTGTTATTTATGAAACGCGATCAGGACAGATAGATCAT 1172
Db 1174 GTGGTTTCAATGTTTACTCTACCTGTAGTGTATGTAAGCACACGAGGACAGATTTGACAA 1233
Qy 1173 TATCTAGGACTTGCATAAAGATTTAAAGATGCTATGGCTAAATCCACGAAATC 1232
Db 1234 TATCTGGGACTTGTGAGGACTCAATAAATGCTGTGTGGCAAGATTCAGGCTAAATC 1293
Qy 1233 CCTGATTTGAAGCGCAAGCTGAAATGAA 1260
Db 1294 CCAGGCGCTAAGAGCGCTGAGTAA 1321

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RESULT 14
US-09-949-016-1127
; Sequence 1127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1127
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1127

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Query Match 12.1%; Score 270.4; DB 4; Length 3202;
Best Local Similarity 67.3%; Pred. No. 5.7e-55;
Matches 382; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

Qy 693 GTTGTGACCTCCTGTTACTGAGAGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 752
Db 1887 GCTATTGACCTGTGTTATTTGGGGGACATCAAGCAGCGGCATCGTTTGGGAGTTTC 1946

Qy 753 CTATTCCTGCTGCTTTCAATGACAGTATTCAGCATTTGACGCTTAACAGCTCAATTGCC 812
Db 1947 CTGCTGCTGCTCTTCTCCTGACCCAGTTTCAGCGTGGTGGCGCTGCTGCGCTACTCGSC 2006

Qy 813 TTGGCCCTGCTCTCTGTGACCATCGCTTTAGGATATACAGGGTGTGATCAAGCTATC 872
Db 2007 CTGGCCGACCTCTCAGCCACCATCATGTTTCCGCATCTCAAGTCTGTGTTTCAAGCAGTG 2066

Qy 873 CAGAAATCAGATGAGGAGCCACCATTCAGGGCATATCTGGAATCTGGAATGCTTATATCT 932
Db 2067 CAGAAACCGAGAGGCCACCCCTTTCAAGGCTACTTTGAGCTTGAGATCACCTTTCT 2126

Qy 933 GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTCTATGTAACACTGCACGATAAAG 992

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Db 2127 CAGAGCAGATTCAGAAAGTACACGAGCTCGCTGCGATTTCTACGTGAACAGCACACTTAAG 2186
Qy 993 GAACCTCAGGCGCCTCTTCTTGTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 1052
Db 2187 GAACCTGAGGAGGCTCTTCTTGTCCAGGACCTGTGTGATTTCTTAAATTTGCAGTCTG 2246
Qy 1053 ATGTGGGTATTTACTATGTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTTGGCT 1112
Db 2247 ATGTGGCTCTGACCTACCTTGTGGGCTCTCTTCAATGGCTGACCCCTGCTCATGGCT 2306
Qy 1113 CTCAATTCACCTCTTCAGTGTTCCTGTTATTTATGAACGGATCAGGACAGATAGATCAT 1172
Db 2307 GTGGTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACAGGACAGATTTGACCA 2366
Qy 1173 TATCTAGGACTTGCATAAAGATTTTAAAGATGCTATGGCTAAATCCACGAAATC 1232
Db 2367 TATCTGGGACTTGTGAGGACTCAATAAATGCTGTGTGGCAAGATTCAGGCTAAATC 2426
Qy 1233 CCTGATTTGAAGCGCAAGCTGAAATGAA 1260
Db 2427 CCAGGCGCTAAGAGCGCACGCTGAGTAA 2454

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RESULT 15
US-09-439-313-279
; Sequence 279, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-279

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Query Match 11.7%; Score 263; DB 3; Length 301;
Best Local Similarity 97.7%; Pred. No. 8.6e-54;
Matches 298; Conservative 0; Mismatches 2; Indels 5; Gaps 3;

Qy 1707 AAAGCAGGAATGACAAAGCTTGTCTTCTGATGTTCTAGGTGATTTGAGCTTTTACT 1766
Db 1 AAAGCAGGAATGACAAAGCTTGTCTTCTGATGTTCTAGGTGATTTGAGCTTTTACT 60

Qy 1767 GTTATATTAATGCGCAATATAAGTAAATATAGATATATATATAGTATGTTTCAAAAGC 1826
Db 61 GTTATATTAATGCGCAATATAAGTAAATATAGATATATATATAGTATGTTTCAAAAGC 120

Qy 1827 TTAGACCTTTACCTTCCAGCCACCCACAGTCTTGTATTTTCAAGAGTCAGTCAATGTT 1886
Db 121 TTAGACCTTTACCTTCCAGCCACCCACAGTCTTGTATTTTCAAGAGTCAGTCAATGTT 180

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QY 1887 ATACATGTGTAGTTCCTCAAGGCACATAAGCTAGAAAGAAATATTTCTA-GGAGCACTAC 1945
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 ATACATGTGTAGTTCCTCAAGGCACATAAGCTAGAAANANAATATTTCTAGGGAGCACTAC 240
QY 1946 CATCTGTTTTCAACATGAAATGCCACACACATAGAACTCCCAACACATCAATTTCAATTGC 2005
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CATCTGTTTTC-ACATGAAATGCCACACACATAGAACTC---CAACATCAATTTCAATTGC 296
QY 2006 ACAGA 2010
Db |||||
297 ACAGA 301

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: August 1, 2005, 10:33:13 ; Search time 9328 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2225	99.3	2332	9	AY102277 Homo sapi
3	2189	97.7	2276	9	AF132047 Homo sapi
4	2158	96.3	2389	9	AY102278 Homo sapi
5	1892.8	84.5	2052	9	AB015639 Homo sapi
6	1615	72.1	1728	9	BC068991 Homo sapi
7	1607.4	71.8	1610	6	BD231889 Homo sapi
8	1601	71.5	1668	9	BC026788 Homo sapi
9	1599	71.4	1619	9	AK129806 Homo sapi
10	1591.2	71.0	1654	9	BC012619 Homo sapi
11	1586.4	70.8	1694	6	CQ783030 Sequence
12	1586.4	70.8	1694	6	BD127437 Primer fo
13	1586.4	70.8	1694	9	AK075039 Homo sapi
14	1577.4	70.4	1599	6	CQ769577 Sequence
15	1574	70.3	1709	9	AB040463 Homo sapi
16	1549	69.2	1700	9	AF177332 Homo sapi
17	1548	69.1	1784	9	BC016165 Homo sapi
18	1536.4	68.6	1698	9	BC014366 Homo sapi
19	1534	68.5	1800	9	AY102276 Homo sapi

20	1533	68.4	4060	9	AY123250
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22	1533	68.4	4102	9	AY123245
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24	1533	68.4	4123	9	AY123247
25	1533	68.4	4160	9	AY123246
26	1533	68.4	4789	6	CQ874017
27	1533	68.4	4789	9	AY102279
28	1525.2	68.1	4822	6	AR220865
29	1512	67.5	1691	9	AF132048
30	1505.4	67.2	1525	9	AK130812
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33	1409	62.9	4632	9	AF148537
34	1383.4	61.8	1466	9	BC071848
35	1319.8	58.9	2162	9	AB049853
36	1199.6	53.6	1206	9	AK172726
37	1122	50.1	1122	6	BD249448
38	1122	50.1	1122	9	HS251384
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40	1090.8	48.7	2410	10	BC070879
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43	1057	47.2	2782	10	AY164741
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ALIGNMENTS

RESULT 1
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LOCUS AF148538 2235 bp mRNA linear PRI 09-SEP-2000
DEFINITION Homo sapiens reticulon 4b mRNA, complete cds.
ACCESSION AF148538
VERSION AF148538.1 GI:10039552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2235)
AUTHORS Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping
JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE 20237542
PUBMED 10773680
REFERENCE 2 (bases 1 to 2235)
AUTHORS Zhou,Y., Yu,L. and Zhao,S.Y.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433, P.R.China

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CDS

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Db 2165 CTAATCTGTTGAATGATTTGTAAGCTGTAAGCTGTAAGCTGTAAGCTGTAAGCTGTAAGCT 2224

Qy 2221 TAAAAAATAA 2231

Db 2225 TAAAAAATAA 2235

RESULT 2

AY102277

LOCUS AY102277 2332 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform B1 (RTN4) mRNA, complete cds; alternatively spliced.

ACCESSION AY102277

VERSION AY102277.1 GI:26800561

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2332)

AUTHORS Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.

TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 2332)

AUTHORS Oertle, T. and Schwab, M.E.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

REFERENCE 3 (bases 1 to 2332)

AUTHORS Van der Putten, H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

FEATURES

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/evidence="experimental"

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AUTHORS	Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.	
TITLE	Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4	
JOURNAL	J. Mol. Biol. 325 (2), 299-323 (2003)	
MEDLINE	23376540	
PUBMED	12488097	
REFERENCE	2 (bases 1 to 2389)	
AUTHORS	Oertle, T. and Schwab, M.E.	
TITLE	Direct Submission	
JOURNAL	Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	
REFERENCE	3 (bases 1 to 2389)	
AUTHORS	Van der Putten, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland	
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VERSION AB015639.1 GI:5821139
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2052)
AUTHORS Yutsudo,M.
TITLE Isolation of a cell death-inducing gene
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 2052)
AUTHORS Yutsudo,M.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka
565-0871, Japan (E-mail:yutsudo@biken.osaka-u.ac.jp,
Tel:81-6-879-8313, Fax:81-6-879-8315)
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REFERENCE
1 (bases 1 to 1728)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Udwin,T.B., Toshitaki,S.,
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Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
AUTHORS
TITLE
JOURNAL

REFERENCE
2 (bases 1 to 1728)
Strausberg, R.
Direct Submission

Submitted (05-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prähbu, Parvaneh Saeedi, JR Santos, Angelique Schmerch, Ursula Skalska, Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 54 Row: c Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28557782
This clone has the following problem: The cds is short compared to the longest cds in the locus.

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ORIGIN

Query Match

Best Local Similarity 72.1%; Score 1615; DB 9; Length 1728;

100.0%; Pred. No. 3.4e-270;

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DEFINITION BD231889
ACCESSION BD231889
VERSION BD231889.1 GI:33041659
KEYWORDS JP 2002511231-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Lin, H. and Cao, L.
TITLE Bone marrow secreted proteins and polynucleotides
JOURNAL Patent: JP 2002511231-A 3 16-APR-2002;
CHIRON CORP
COMMENT OS Homo sapiens (human)
PN JP 2002511231-A/3
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PI HAISHAN LIN, LI CAO
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TITLE

JOURNAL
PUBLISHED

REFERENCE

2 (bases 1 to 1668)

Direct Submission

AUTHORS

JOURNAL

REMARK

COMMENT

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 1668)
 Strausberg, R.
 Direct Submission
 Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-f@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 21 Row: h Column: 13
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
 This clone has the following problem: The cds is short compared to the longest cds in the locus.

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ORIGIN

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ACCESSION AKI29806.1 GI:34526422
VERSION oligo capping; fis (full insert sequence).
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y.,
Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M.,
Sugiyama, T., Irie, R., Otsuki, F., Sato, H., Nishikawa, T.,
Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
1 Unpublished
2 (bases 1 to 1619)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: fildna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB, clone selection for
full insert sequencing: RAB and Helix Research Institute.
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IMAGE:4082756)			
ACCESSION	BC012619		
VERSION	BC012619.1 GI:15214977		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
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REFERENCE	1 (bases 1 to 1654)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,		

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1654)
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbio.org
 Anup Madan, Jessica Fahey, Brian Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
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 Series: IRAL Plate: 19 Row: d Column: 8
 This clone was selected for full length sequencing because it
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 This clone has the following problem: The cds is short compared to
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RESULT 11
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 REFERENCE 1
 AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
 Koga, H.
 TITLE Primers for synthesizing full length cDNA clones and their use
 JOURNAL Patent: EP 1396543-A 3170 10-MAR-2004;
 Research Association for Biotechnology (JP)
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 Query Match 70.8%; Score 1586.4; DB 6; Length 1694;
 Best Local Similarity 99.9%; Pred. No. 3.1e-265;

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LOCUS	BD127437		
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD127437		
VERSION	BD127437.1	GI:23222382	
KEYWORDS	JP 2002017375-A/2868		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1694)		
	Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and Koga, H.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002017375-A 2868 22-JAN-2002;		
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017375-A/2868 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253172 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO ISHII, PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA, PI TETSUJI OTSUKI,HISASHI KOGA PC C12N1/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key FT CDS Location/Qualifiers (479)..(1351).		
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QY	181	GCCACACCGCCGCGCAGCCGCTTCAAGTACCAAGTTCTGTGAGGAGCCCGAGGACGAGG	240
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QY	241	AGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	300
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QY	301	TGGAGAGGAAGCCCGCGCGCGGCTGTCCGGCGGCCAGTCCCAAGTCCCAAGTCCCGCG	360
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QY	660	GCGCCCAAGCGCAGGGGCTCTCGGGCTCAGTGGTGTGACCTCTCTACTTGGAGAGAC	719
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 ACCESSION AK075039
 VERSION AK075039.1 GI:22760874
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

 REFERENCE
 1
 AUTHORS Isegai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuko, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1694)
 AUTHORS Isegai, T. and Otsuki, T.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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FEATURES

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 Best Local Similarity 99.9%; Pred. No. 3.1e-265;
 Matches 1598; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGTCACACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACCC 60
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ACCESSION AB040463
VERSION AB040463.1 GI:11610576
KEYWORDS reticulon.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity
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MEDLINE
PUBMED 11126360
REFERENCE
2 (bases 1 to 1709)
Eguchi,Y., Tagami,S. and Tsujimoto,Y.
Direct Submission
TITLE Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
JOURNAL School of Medicine, Biomedical Research Center, Department of

Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
(E-mail:eguchi@gen.med.osaka-u.ac.jp, Tel: +81-6-6879-3363,
Fax: +81-6-6879-3369)

FEATURES

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Location/Qualifiers

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Best Local Similarity 99.4%; Pred. No. 4.4e-263;

Matches 1593; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

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Title: US-09-544-776-1
Perfect score: 2240
Sequence: 1 cgtcacacagtggtccct.....taaaaaaaaaaaaaaaaaa 2240

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2238.4	99.9	2240	3 AAC64406	AAC64406 Human Nog
2	2231	99.6	2235	6 ABV94681	ABV94681 Human pan
3	1892.8	84.5	2052	6 ABK90133	ABK90133 DNA encod
4	1607.4	71.8	1610	3 AAZ36230	AAZ36230 cDNA enco
5	1586.4	70.8	1694	4 AAK94408	AAK94408 Human ful
6	1586.4	70.8	1694	12 ADL31137	ADL31137 Full leng
7	1581	70.4	1758	4 AAF32725	AAF32725 Human sec
8	1577.4	70.4	1599	10 ADI62860	ADI62860 Human apo
9	1533	68.4	4789	13 ADR83534	ADR83534 Human ret
10	1525.2	68.1	4822	6 ABS70449	ABS70449 Human bon
11	1488.8	66.5	1798	6 ABK90135	ABK90135 DNA encod
12	1473.4	65.8	1514	6 ABK34580	ABK34580 Human cdn
13	1464.6	65.4	1683	4 AAD08386	AAD08386 Human sec
14	1409	62.9	4632	6 ABV94680	ABV94680 Human pan
15	1409	62.9	4632	10 ADG32772	ADG32772 Human DNA
16	1359.2	60.7	1785	12 ADK14166	ADK14166 Human aut
17	1325	59.2	4698	8 ABX34563	ABX34563 Human mdd
18	1216	54.3	1216	6 ABA05903	ABA05903 Human RTN
19	1122	50.1	1122	3 AAZ56888	AAZ56888 Human MAG
20	1122	50.1	1122	4 AAF90325	AAF90325 Human NOG

21	1097.6	49.0	2610	11 ADI31056	ADI31056 Human CDN
22	1057	47.2	2782	10 ADB5284	ADB5284 Rat fooc
23	1033.4	46.1	3833	3 AAD01174	AAD01174 Bovine ne
c 24	1010.2	45.1	4710	4 AAL04697	AAL04697 Human rep
c 25	1010.2	45.1	4710	4 ABL97604	ABL97604 Human tes
26	924.4	41.3	1213	2 AAX04379	AAX04379 Human sec
27	923	41.2	4093	3 AAZ3454	AAZ3454 cDNA enco
28	907	40.5	3919	12 ADF45550	ADF45550 Human Nog
29	907	40.5	4053	4 AAS09453	AAS09453 Human CDN
30	907	40.5	4053	9 ACC81048	ACC81048 Human Nog
31	907	40.5	4053	12 ADP13574	ADP13574 Renal cel
32	906.8	40.5	994	12 ADP18854	ADP18854 Human sec
33	904.4	40.4	991	2 AAX97587	AAX97587 Extended
34	904.2	40.4	1980	4 AAI98079	AAI98079 Human neu
35	902	40.3	972	10 ADG63407	ADG63407 Partial h
36	883	39.4	2386	2 AAV30920	AAV30920 Human sec
37	879.8	39.3	2386	5 AAF98399	AAF98399 Human CDN
38	800	35.7	3535	4 AAH72837	AAH72837 Human cer
39	755.8	33.7	4684	3 AAD01173	AAD01173 Rat neuro
40	751.8	33.6	4684	6 ABN86600	ABN86600 Rat neuro
41	683.6	30.5	1568	3 AAD01175	AAD01175 Rat neuro
42	682	30.4	799	2 AAV23695	AAV23695 Human NSP
43	658	29.4	770	3 AAA72983	AAA72983 Human NSP
c 44	610.4	27.2	3413	6 ABZ78047	ABZ78047 Human bre
45	605.8	27.0	2934	12 ADQ16433	ADQ16433 Construct

ALIGNMENTS

RESULT 1	
AAC64406	
ID AAC64406 standard; cDNA; 2240 BP.	
XX AAC64406;	
AC AAC64406;	
XX 08-FEB-2001 (first entry)	
XX Human Nogo B nucleotide sequence SEQ ID NO:1.	
XX Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;	
KW stress-phosphorylated endoplasmic reticulum protein; cytosolic;	
KW gene therapy; cell growth; cellular stress response; neuron growth;	
KW regulator of oxidative stress; inhibitor of neurite outgrowth;	
KW axon regeneration; diagnosis; cancer; identification; ss.	
OS Homo sapiens.	
XX WO200060083-A1.	
XX 12-OCT-2000.	
XX 07-APR-2000; 2000WO-US009383.	
XX 08-APR-1999; 99US-0128372P.	
PR 21-JUN-1999; 99US-0140331P.	
XX (CHIR) CHIRON CORP.	
XX Wei D, Halenbeck R, Williams LT;	
XX WPI; 2000-665007/64.	
DR P-PSDB; AAB24242.	
XX Novel protein associated with cell stress response useful for modulating	
PT stress levels, cell growth, diagnosis and treatment of cancer and	
PT malignant growth and for identifying agonists and antagonists.	
XX Claim 2; Page 63-64; 68pp; English.	
XX The present sequence encodes a human stress-phosphorylated endoplasmic	
CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and	
CC is a modulator of the storage and exchange of calcium, cell growth and	

QY 841 TTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 900
DB 845 TTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 904
QY 901 GGGCATATCTGGATCTGAAGTGTGATATCTGAGGAGTGGTTCAGAAATGACAGTAAT 960
DB 905 GGGCATATCTGGATCTGAAGTGTGATATCTGAGGAGTGGTTCAGAAATGACAGTAAT 964
QY 961 CTGCTCTGGTCACTGTAAGTGCAGATAAAGAACTCAGAGCGCTCTCTCTAGTTGATG 1020
DB 965 CTGCTCTGGTCACTGTAAGTGCAGATAAAGAACTCAGAGCGCTCTCTCTAGTTGATG 1024
QY 1021 ATTTAGTTGATCTCTGAAGTTTGCAGTGTGATGTTGGGTATTTACCTATGTTGGTGCCT 1080
DB 1025 ATTTAGTTGATCTCTGAAGTTTGCAGTGTGATGTTGGGTATTTACCTATGTTGGTGCCT 1084
QY 1081 TGTTAATGGTCTGACACTGATGATTTTGGCTCTCAATTTCACTCTTCACTGTTCTGTTA 1140
DB 1085 TGTTAATGGTCTGACACTGATGATTTTGGCTCTCAATTTCACTCTTCACTGTTCTGTTA 1144
QY 1141 TTTATGAACGGCATCAGGCACAGATAGATCAATATCTAGGACTTGCAAAATGAAGTGTTA 1200
DB 1145 TTTATGAACGGCATCAGGCACAGATAGATCAATATCTAGGACTTGCAAAATGAAGTGTTA 1204
QY 1201 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAATGAA 1260
DB 1205 AAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAATGAA 1264
QY 1261 AACGCCCAAAATTAATAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATATACGG 1320
DB 1265 AACGCCCAAAATTAATAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATATACGG 1324
QY 1321 GGGAGGGTCAGGGAAGAACCTTTGACGTTGACGTCAGTTCACAGATCGTTGTTAG 1380
DB 1325 GGGAGGGTCAGGGAAGAACCTTTGACGTTGACGTCAGTTCACAGATCGTTGTTAG 1384
QY 1381 ATCTTTATTTTGTAGCCATGCACTGTGTGAGGAAAAATTAACCTGTCTTGACTGCCATGTG 1440
DB 1385 ATCTTTATTTTGTAGCCATGCACTGTGTGAGGAAAAATTAACCTGTCTTGACTGCCATGTG 1444
QY 1441 TTCATCATCTTAAGTATTTGTAAGCTGTATGTAAGGATTTAAACCGTAAATCATATCTTTT 1500
DB 1445 TTCATCATCTTAAGTATTTGTAAGCTGTATGTAAGGATTTAAACCGTAAATCATATCTTTT 1504
QY 1501 TCCTATCTGAGCACTGTGTGGAATAAAAAACCTGTATATTTTACTTTCTGTCAGATAGTC 1560
DB 1505 TCCTATCTGAGCACTGTGTGGAATAAAAAACCTGTATATTTTACTTTCTGTCAGATAGTC 1564
QY 1561 TTGCGCATCTTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAAGCCCT 1620
DB 1565 TTGCGCATCTTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAATAAAAAAGCCCT 1624
QY 1621 TTTCAGTTTGTGCACTGTATGTCCTGTAGATTTGATGAGATTTTCTGAAATGAAT 1680
DB 1625 TTTCAGTTTGTGCACTGTATGTCCTGTAGATTTGATGAGATTTTCTGAAATGAAT 1684
QY 1681 GTTTGTTTGTAGCAGATCATACCGGTAAAGAGGAATGACAAAGCTGCTTTCTGTTAT 1740
DB 1685 GTTTGTTTGTAGCAGATCATACCGGTAAAGAGGAATGACAAAGCTGCTTTCTGTTAT 1744
QY 1741 GTTCTAGTGTATTTGACTTTTACTGTTATATTAATTTGCCAATATAAGTAATATAGAT 1800
DB 1745 GTTCTAGTGTATTTGACTTTTACTGTTATATTAATTTGCCAATATAAGTAATATAGAT 1804
QY 1801 TATATATGTATAGTTTTCACAAAGCTTAGACCTTTTACCTTCCAGGCCACCCACAGTGTCT 1860
DB 1805 TATATATGTATAGTTTTCACAAAGCTTAGACCTTTTACCTTCCAGGCCACCCACAGTGTCT 1864
QY 1861 TGATATTTTCAGAGTCAGTCAATTTGGTTATACATGTTAGTTCCTCAAGCAGATAGCTAGAA 1920
DB 1865 TGATATTTTCAGAGTCAGTCAATTTGGTTATACATGTTAGTTCCTCAAGCAGATAGCTAGAA 1924

QY 1921 GAAGAAATATTTCTAGAGCACTACCATCTGTTTCAACATGAATGCCACACATAGA 1980
DB 1925 GAAGAAATATTTCTAGAGCACTACCATCTGTTTCAACATGAATGCCACACATAGA 1984
QY 1981 ACTCCAAACATCAATTTCAATTCACAGACTGACTGTAGTTAAATTTTGTTCACAGAACT 2040
DB 1985 ACTCCAAACATCAATTTCAATTCACAGACTGACTGTAGTTAAATTTTGTTCACAGAACT 2044
QY 2041 ATGACTGAATCTAATGCTTCCAAAAATGTTTGTGCAAAATATCAAAATGTTTAT 2100
DB 2045 ATGACTGAATCTAATGCTTCCAAAAATGTTTGTGCAAAATATCAAAATGTTTAT 2104
QY 2101 GCAAGAAATTAATTAATTAACAAAATGAAGATTATACATTGTTGTTAAAGCTGACTGAA 2160
DB 2105 GCAAGAAATTAATTAATTAACAAAATGAAGATTATACATTGTTGTTAAAGCTGACTGAA 2164
QY 2161 CTAAATCTGTGGAATGCAATGCTGAACTGTAAAGCAAGATATCAATAAAGCTTATAGACT 2220
DB 2165 CTAAATCTGTGGAATGCAATGCTGAACTGTAAAGCAAGATATCAATAAAGCTTATAGACT 2224
QY 2221 TAAAAAATAA 2231
DB 2225 TAAAAAATAA 2235
RESULT 3
ABK90133
ID ABK90133 standard; DNA; 2052 BP.
XX AC ABK90133;
XX DT 21-OCT-2002 (first entry)
XX DE DNA encoding human NogoB protein.
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;
KW Nogo-associated disease; metastasis; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
CDS 67..1188
FT /*tag= a
FT /product= "Human NogoB protein"
XX WO200257483-A2.
XX PD 25-JUL-2002.
XX PF 18-JAN-2002; 2002WO-GB000228.
XX PR 18-JAN-2001; 2001GB-00001312.
XX PA (GLAX) GLAXO GROUP LTD.
XX PA (SMK) SMITHLINE BEECHAM PLC.
XX PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX WPI; 2002-599722/64.
XX P-PSDB; ABG30937.
XX PT Identifying modulators of Nogo or BACE activity for treating acute
XX PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
XX PT providing and monitoring interaction between Nogo and BACE polypeptides.
XX PS Disclosure; Page 50-52; 68pp; English.
XX CC The present invention relates to a new method of identifying modulators
of Nogo function or BACE activity. The method involves providing Nogo and

Qy	1866	TTTCAGAGTCAGTCATTTGGTTTATACATGTGTAGTTCCTCAAGCACAATTAAGCTTAGAAGAAGA	1925
Db	1700	TTTCAGAGTCAGTCATTTGGTTTATACATGTGTAGTTCCTCAAGCACAATTAAGCTTAGAAGAAGA	1759
Qy	1926	AATATTCTTAGGAGCAGTACCATCTGTGTTTCAACATCAATGAAATGCCACACACATAGAACTCC	1985
Db	1760	AATATTCTTAGGAGCAGTACCATCTGTGTTTCAACATCAATGAAATGCCACACATAGAACTC-	1818
Qy	1986	AACAACATCAATTTTCATTGTCACAGACTGACTGTAGTTAAATTTTGTCA CAGAATCTATGGA	2045
Db	1819	--CAACATCAATTTTCATTGTCACAGACTGACTGTAGTTAAATTTTGTCA CAGAATCTATGGA	1876
Qy	2046	CTGAATCTAATGCTTCCAAAATGTTGTTTGTGGCAAAATATCAAAACATTTGTTATGCAAG	2105
Db	1877	CTGAATCTAATGCTTCCAAAATGTTGTTTGTGGCAAAATATCAAAACATTTGTTATGCAAG	1936
Qy	2106	AAATTATTAAATTACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAACTAAA	2165
Db	1937	AAATTATTAAATTACAAAATGAAGATTTATACCATTTGTGGTTTAAAGCTGTACTGAACTAAA	1996
Qy	2166	TCGTGGAATGCATTTGTGAACCTGTAAAGCAAGATTCAAATPAAGCTTTATAGACTT	2221
Db	1997	TCGTGGAATGCATTTGTGAACCTGTAAAGCAAGATTCAAATPAAGCTTTATAGACTT	2052

RESULT 4
AAZ36230
ID AAZ36230 standard; cDNA; 1610 BP.
XX
XX AAZ36230;
XX AC
XX AC
XX DT 22-FEB-2000 (first entry)
XX
XX cDNA encoding a bone marrow secreted protein designated BMS112.
XX
XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint; ss.
KW

XX	Homo sapiens.	
OS		
XX		
FX	Key	Location/Qualifiers
FT	CDS	132..1253
FT		/*tag= a
FT		/product= "bone marrow secreted protein"
FT		1516..1521
FT		/*tag= b
FT	polyA_signal	

XX	WO9933979-A2.
PN	
XX	
PD	08-JUL-1999.
XX	
XX	
PF	18-DEC-1998; 98WO-US027008.
XX	
PR	30-DEC-1997; 97US-0068958P.
PR	24-SEP-1998; 98US-0101603P.
PR	30-SEP-1998; 98US-0102540P.
XX	
PA	(CHIR) CHIRON CORP.

PI Lin H, Cao L;
XX WPI; 2000-038344/03.
DR P-PSDB; AAY53624.
DR

3.

PT New isolated human polynucleotide and secreted proteins can induce
 PR production of other cytokines in certain cell populations.
 XX
 XX
 XX Claim 11; Page 72-74; 120pp; English.
 CC AAZ36228-49 encode bone marrow secreted proteins of human bone marrow
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 CC cell differentiation activity (either inducing or inhibiting). They can
 CC be used to support colony forming cells or factor-dependent cell lines,
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 CC deficiencies. In addition, they may be used to support the growth and
 CC proliferation of erythroid progenitor cells, and to treat various
 CC anaemias. They can have colony stimulating factor (CSF) activity and can
 CC be used to support the growth and proliferation of myeloid cells such as
 CC granulocytes, monocytes or macrophages, to prevent or treat myelo-
 CC suppression, to support the growth and proliferation of megakaryocytes
 CC and platelets, thereby allowing prevention or treatment of platelet
 CC disorders such as thrombocytopenia, to support the growth and
 CC proliferation of hematopoietic stem cells, either in place of or in
 CC conjunction with platelet transfusions, to treat stem cell disorders,
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 CC repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances where
 CC bone is not normally formed and thus have an application in healing bone
 CC fractures and cartilage damage or defects, prophylactic use in fracture
 CC reduction and also in the improved fixation of artificial joints
 XX
 XX Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 U; 0 Other;

Query Match	71.8%	Score 1607.4	DB 3	Length 1610
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1608	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	7	CACAGTAGGTCCCTCGGCTCAGTCCGCCAGCCCTCTCAGTCTCTCCCAACCCCCACA	66	
Db				
Qy	1	CACAGTAGGTCCCTCGGCTCAGTCCGCCAGCCCTCTCAGTCTCTCCCAACCCCCACA	60	
Db				
Qy	67	CCGCCCGCGCTTGTGACCGCGGCCCGCGCGCGGCGAGAGTGTGAGCATCATCTCC	126	
Db				
Qy	61	CCGCCCGCGCTTGTGACCGCGGCCCGCGCGCGGCGAGTGTGAGCATCATCTCC	120	
Db				
Qy	127	ACCTCTCAGCATCGAAGACTGAGCAGTCTCTCTGGTCTCTGTCCTCGACACGCCAC	186	
Db				
Qy	121	ACCTCTCAGCATCGAAGACTGAGCAGTCTCTCTGGTCTCTGTCCTCGACACGCCAC	180	
Db				
Qy	187	CCCGGCCGACCGCCGCTTCAAGTACACAGTTCTGTGAGGGAGCCCGAGGACGAGGAGG	246	
Db				
Qy	181	CCCGGCCGACCGCCGCTTCAAGTACACAGTTCTGTGAGGGAGCCCGAGGACGAGGAGG	240	
Db				
Qy	247	AAGAGGAGGAGGAAGAGGAGGACGAGACGAAGACTTGTGAGAGTGTGAGGTGTGTGAGA	306	
Db				
Qy	241	AAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACTTGTGAGAGTGTGAGGTGTGTGAGA	300	
Db				
Qy	307	GGAGCCCGCGCCCGGCTGTCCGGGCCCCAGTGCACCGCCCTCGCGCCCGCGGCGC	366	
Db				
Qy	301	GGAGCCCGCGCCCGGCTGTCCGGGCCCCAGTGCACCGCCCTCGCGCCCGCGGCGC	360	
Db				
Qy	367	CCCTGATGGACTTCGGAAATGACTTCTGTCCCGCGGCCCGCCCGGGGACCCCTTCGCGCGC	426	
Db				
Qy	361	CCCTGATGGACTTCGGAAATGACTTCTGTCCCGCGGCCCGCCCGGGGACCCCTTCGCGCGC	420	
Db				
Qy	427	CTCCCCCGTGCGCCCGGAGCGGAGCGGTCTTGGGACCCGAGCCCGGTGTGTCGACCG	486	
Db				
Qy	421	CTCCCCCGTGCGCCCGGAGCGGAGCGGTCTTGGGACCCGAGCCCGGTGTGTCGACCG	480	
Db				
Qy	487	TGCCCGCGCATCCCGCTGTCTGCTGCGAGTCTCGCCCTTCCAAGTCTCCCTGAGGACG	546	
Db				
Qy	481	TGCCCGCGCATCCCGCTGTCTGCTGCGAGTCTCGCCCTTCCAAGTCTCCCTGAGGACG	540	
Db				
Qy	547	ACGAGCTCTCGGCCCGGCTCCCTCTCTCCCGCGGCGAGGCTGAGCCCCCAGGCGAGC	606	
Db				

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Db 541 |ACGAGCTCCGGCCCGGCTCCCTCTCTCCCGGCGAGGTGAGCCCGCCAGCAGC 600
Qy 607 |CCGTGTGGAACCCCGCCAGCCCGGCTCCCGCGCGCGCCCCCTCCACCCCGCGCGCCCA 666
Db 601 |CCGTGTGGAACCCCGCCAGCCCGGCTCCCGCGCGCGCCCCCTCCACCCCGCGCGCCCA 660
Qy 667 |AGCCGAGGGGCTCTCCGGGCTCAGTGTGTTGACCTCTCTGTACTGAGAGACATTAAGA 726
Db 661 |AGCCGAGGGGCTCTCCGGGCTCAGTGTGTTGACCTCTCTGTACTGAGAGACATTAAGA 720
Qy 727 |AGACTGAGTGGTGTGTTGGTCCAGCCATATCTCTGCTGCTTTCATTCAGACATTTACGA 786
Db 721 |AGACTGAGTGGTGTGTTGGTCCAGCCATATCTCTGCTGCTTTCATTCAGACATTTACGA 780
Qy 787 |TTGTGAGCGTAAACGCTACATTCCTGTCCTGTCCTCTCTGTGACCATCAGCTTTAGGA 846
Db 781 |TTGTGAGCGTAAACGCTACATTCCTGTCCTGTCCTCTCTGTGACCATCAGCTTTAGGA 840
Qy 847 |TATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 906
Db 841 |TATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCAT 900
Qy 907 |ATCTGGAATCTGAAGTTGCTATATCTGAGGATGGTTTCAGAACTACAGTAATTCGCTC 966
Db 901 |ATCTGGAATCTGAAGTTGCTATATCTGAGGATGGTTTCAGAACTACAGTAATTCGCTC 960
Qy 967 |TTGTCATGTGAACGCAAGCAATGAAGAACTCAGCGGCTCTCTTGTAGTGAATTTAG 1026
Db 961 |TTGTCATGTGAACGCAAGCAATGAAGAACTCAGCGGCTCTCTTGTAGTGAATTTAG 1020
Qy 1027 |TTGATCTCTGAAGTTGCTGAGTGTGATGGGTAATTCATGTTGGTGGCTTGTGTTA 1086
Db 1021 |TTGATCTCTGAAGTTGCTGAGTGTGATGGGTAATTCATGTTGGTGGCTTGTGTTA 1080
Qy 1087 |ATGCTCTGACACTACTGATTTGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATG 1146
Db 1081 |ATGCTCTGACACTACTGATTTGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATG 1140
Qy 1147 |AACGGCATCAGGCACAGATAGATCATTTCTAGGACTTGCATAAAGAAATGTTAAAGATG 1206
Db 1141 |AACGGCATCAGGCACAGATAGATCATTTCTAGGACTTGCATAAAGAAATGTTAAAGATG 1200
Qy 1207 |CTATGGCTAAATCAAGCAAAATCCCTGATTAAGCGCAAGCTGAATGAAGAACGCC 1266
Db 1201 |CTATGGCTAAATCAAGCAAAATCCCTGATTAAGCGCAAGCTGAATGAAGAACGCC 1260
Qy 1267 |CAAAATTAATAGTAGGAGTTTCATCTTTAAAGGGATATTCATTTGATTAACGGGGAGG 1326
Db 1261 |CAAAATTAATAGTAGGAGTTTCATCTTTAAAGGGATATTCATTTGATTAACGGGGAGG 1320
Qy 1327 |GTCAGGGAAGAACGAACCTTGACGTTGACGTCAGTGTTCAGAGATCGTTGTTAGATCTTT 1386
Db 1321 |GTCAGGGAAGAACGAACCTTGACGTTGACGTCAGTGTTCAGAGATCGTTGTTAGATCTTT 1380
Qy 1387 |ATTTTTCAGCATGCACTGTGTTGAGGAAAAATTAACCTGTCTGTCATGTCATGTTTCATC 1446
Db 1381 |ATTTTTCAGCATGCACTGTGTTGAGGAAAAATTAACCTGTCTGTCATGTCATGTTTCATC 1440
Qy 1447 |ATCTTAAGTATTTAAGCTGTATGATGATGATTTTAAACCGTAATCATATCTTTTCTAT 1506
Db 1441 |ATCTTAAGTATTTAAGCTGTATGATGATGATTTTAAACCGTAATCATATCTTTTCTAT 1500
Qy 1507 |CTGAGGCATCTGGTGAATAAAAAACCTGTATATTTTACTTTGTTGTCAGATAGTCTGCGG 1566
Db 1501 |CTGAGGCATCTGGTGAATAAAAAACCTGTATATTTTACTTTGTTGTCAGATAGTCTGCGG 1560
Qy 1567 |CATCTTGGCAAGTTGCGAGATGGTGGAGCTAGAAAAAAGAAAAA 1615
Db 1561 |CATCTTGGCAAGTTGCGAGATGGTGGAGCTAGAAAAAAGAAAAA 1609
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RESULT 5

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AAK94408
ID AAK94408 standard; cDNA; 1694 BP.
XX
AC AAK94408;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 3170.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; es.
XX
OS Homo sapiens.
XX
PN EF1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
(HELI-) HELIX RES INST.
XX
PA Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
DR WPI; 2001-524255/58.
DR P-PSDB; AAM93484.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO
XX
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;
Query Match 70.8%; Score 1586.4; DB 4; Length 1694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CGTCACACAGTAGTCCCTCGGCTCAGTCCGCGCCAGCCCTCTCAGTCTCTCCCAACC 60
Db 95 CGTCACACAGTAGTCCCTCGGCTCAGTCCGCGCCAGCCCTCTCAGTCTCTCCCAACC 154
Qy 61 CCACACCGCCCGGCTCTGAGACCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCATC 120
Db 155 CCACACCGCCCGGCTCTGAGACCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCATC 214
Qy 121 ATCTCCACCTCCAGCCATGGAAGACCTGGAACAGTCTCTCTGCTCTGCTCTCGGACA 180
Db 215 ATCTCCACCTCCAGCCATGGAAGACCTGGAACAGTCTCTCTGCTCTGCTCTCGGACA 274
Qy 181 GCCACACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 240
Db 275 GCCACACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 334
Qy 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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Qy 1 CGTCACACAGTAGTCCCTGGCTCAGTCGGCCAGCCCTCTCAAGTCTCTCCCAACC 60
Db |||
Qy 95 CGTCACACAGTAGTCCCTGGCTCAGTCGGCCAGCCCTCTCAAGTCTCTCCCAACC 154
Db |||
Qy 61 CCACAAACCGCCCGGCTCTGAGACGGCCCGCGCGCGCGCGCAGCTGCGACATC 120
Db |||
Qy 155 CCACAAACCGCCCGGCTCTGAGACGGCCCGCGCGCGCGCGCAGCTGCGACATC 214
Db |||
Qy 121 ATCTCCACCTCTCAGCACTGAGCAAGCTGAGCAAGCTCTCTCTGGTCTCTCTCGGACA 180
Db |||
Qy 215 ATCTCCACCTCTCAGCACTGAGCAAGCTGAGCAAGCTCTCTCTGGTCTCTCTCGGACA 274
Db |||
Qy 181 GCCACACCGCCCGCAGCCCGCTCAAGTACCAAGTTCGTGAGGGCCCGAGGACGAGG 240
Db |||
Qy 275 GCCACACCGCCCGCAGCCCGCTCAAGTACCAAGTTCGTGAGGGCCCGAGGACGAGG 334
Db |||
Qy 241 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db |||
Qy 335 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 394
Db |||
Qy 301 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db |||
Qy 395 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454
Db |||
Qy 361 GCGCGCCCTGATGAGACTTCGGAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCG 420
Db |||
Qy 455 GCGCGCCCTGATGAGACTTCGGAATGACTTCGTGCGCGCGCGCGCGCGCGCGCGCG 514
Db |||
Qy 421 CGGCGCTCTCCCGCG -TCGCCCGCGAGCGGAGCGCTCTTGGAGACCGAGCGCGGTGCG 479
Db |||
Qy 515 CGGCGCTCTCCCGCGTTCGCCCGCGAGCGGAGCGCTCTTGGAGACCGAGCGCGGTGCG 574
Db |||
Qy 480 TCAGACCGTCCCGCGCATCCCGCTGTCTGTCTGCTGCGCGAGCTCTCGCCCTCCAGCTCCCT 539
Db |||
Qy 575 TCAGACCGTCCCGCGCATCCCGCTGTCTGTCTGCTGCGCGAGCTCTCGCCCTCCAGCTCCCT 634
Db |||
Qy 540 GAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
Db |||
Qy 635 GAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
Db |||
Qy 600 GCAGAGCCCGTGGAGCCCGCGAGCGCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCG 659
Db |||
Qy 695 GCAGAGCCCGTGGAGCCCGCGAGCGCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCG 754
Db |||
Qy 660 GCGCCCAAGCGCAGCGGCTCTCGGGCTCAGTGGTGTGACCTCTCTGTACTGAGAGAGAC 719
Db |||
Qy 755 GCGCCCAAGCGCAGCGGCTCTCGGGCTCAGTGGTGTGACCTCTCTGTACTGAGAGAGAC 814
Db |||
Qy 720 ATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Db |||
Qy 815 ATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
Db |||
Qy 780 TTCAGCATTTGAGGTAACAGCTACATGTCCTTGGCCCTGCTCTGTGACCATCAGC 839
Db |||
Qy 875 TTCAGCATTTGAGGTAACAGCTACATGTCCTTGGCCCTGCTCTGTGACCATCAGC 934
Db |||
Qy 840 TTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCATTC 899
Db |||
Qy 935 TTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCATTC 994
Db |||
Qy 900 AGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGAGTACAGTAAT 959
Db |||
Qy 995 AGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGAGTACAGTAAT 1054
Db |||
Qy 960 TCTGCTCTTGTGCTGATGAACTGACGATTAAGAACTCAGCGCCCTCTTCTAGTTGAT 1019
Db |||
Qy 1055 TCTGCTCTTGTGCTGATGAACTGACGATTAAGAACTCAGCGCCCTCTTCTAGTTGAT 1114
Db |||
Qy 1020 GATTAGTTGATTTCTGAAAGTTTGCAGTGTGTGATGTGGGTATTTTACATGTGTGGTGCC 1079
Db |||
Qy 1115 GATTAGTTGATTTCTGAAAGTTTGCAGTGTGTGATGTGGGTATTTTACATGTGTGGTGCC 1174
Db |||
Qy 1080 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCAATTTCACTCTTTCAGTGTTCCTGTT 1139
Db |||
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Db |||
Qy 1175 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCAATTTCACTCTTCAAGTTCCTGTT 1234
Db |||
Qy 1140 ATTATGAAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAATAAGAAATGTT 1199
Db |||
Qy 1235 ATTATGAAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAATAAGAAATGTT 1294
Db |||
Qy 1200 AAAGATGCTATGCTTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGA 1259
Db |||
Qy 1295 AAAGATGCTATGCTTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGA 1354
Db |||
Qy 1260 AAAGCGCCAAATAATTTAGTAGGAGTTTCATCTTTTAAAGGGGATATTCAATTTGATTATACG 1319
Db |||
Qy 1355 AAAGCGCCAAATAATTTAGTAGGAGTTTCATCTTTTAAAGGGGATATTCAATTTGATTATACG 1414
Db |||
Qy 1320 GGGGAGGGTCTCAGGGAAGAACGAAACCTTGACGTTTGCAGTGCAGTTTTCACAGATCGTTGTTA 1379
Db |||
Qy 1415 GGGGAGGGTCTCAGGGAAGAACGAAACCTTGACGTTTGCAGTGCAGTTTTCACAGATCGTTGTTA 1474
Db |||
Qy 1380 GATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAATTAACCTTCTTGAATGCCATGT 1439
Db |||
Qy 1475 GATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAATTAACCTTCTTGAATGCCATGT 1594
Db |||
Qy 1440 GTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATTTTAAACCTTAATCATATCTTT 1499
Db |||
Qy 1535 GTTCATCATCTTAAGTATTTGTAAGCTGCTATGATGATTTTAAACCTTAATCATATCTTT 1594
Db |||
Qy 1500 TTCTATCTCAGGCACCTGGTGGAAATAAAAAACCTGTATATTTTACTTTTGTGCAGATAGT 1559
Db |||
Qy 1595 TTCTATCTCAGGCACCTGGTGGAAATAAAAAACCTGTATATTTTACTTTTGTGCAGATAGT 1654
Db |||
Qy 1560 CTTGCCGCACTTTGGCAAGTTGCAGATGCTGGAGCTAG 1599
Db |||
Qy 1655 CTTGCCGCACTTTGGCAAGTTGCAGATGCTGGAGCTAG 1694
Db |||
```

RESULT 7

AAF32725/c
ID AAF32725 standard; cDNA; 1758 BP.

XX AAF32725;

XX 23-MAR-2001 (first entry)

XX Human secreted protein gene 27 SEQ ID NO:37.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;
XX angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;
XX ocular disorder; corneal infection; wound healing; food additive;
XX preservative; ss.

XX Homo sapiens.

XX OS

XX WO200077255-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000MO-US014926.

XX 11-JUN-1999; 99US-0138628P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-025337/03.

XX P-PSDB; AAB64448.

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

Claim 1; Page 495; 593pp; English.

The polynucleotide sequences given in AAF32699 to AAF32747 encode the human secreted proteins given in AAB64422 to AAB64470. AAB64471 to AAB64548 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antireumatic; antiproliferative; cycostatic; cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAF32690 to AAF32698 and AAB64421 represent sequences used in the exemplification of the present invention

Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;

Query Match	70.6%;	Score 1581;	DB 4;	Length 1758;
Best Local Similarity	96.5%;	Pred. No. 0;		
Matches 1661;	Conservative	0;	Mismatches	0;
Indels	60;	Gaps	2;	
QY	577	CCCCGGCCAGGTGAGCCCCCAGGACAGACCCGGTGTGACCCCGCCAGCCCGCGCTCCCG	636	
DB	1750	CCCCGGCCAGGTGAGCCCCCAGGACAGACCCGGTGTGACCCCGCGCTCCCG	1691	
QY	637	CCGGCCCCCCTCCACCCCGCGCCGCGCCAGGCGCAGGGGCTCTCGGGCTCAGTG----	692	
DB	1690	CCGGCCCCCCTCCACCCCGCGCCGCGCCAGGCGCAGGGGCTCTCGGGCTCAGTGGATG	1631	
QY	693	-----GTTGTTG	699	
DB	1630	AGACCCCTTTTCTCTCTCTGTCATCTGAGCCCTGTGATACGCTCTCTGACGTTGTTG	1571	
QY	700	ACCTCCTGTACTGGAGACATTAAGAGATGGAGTGGTCTTTGGTGCCAGCCCTATTCC	759	
DB	1570	ACCTCCTGTACTGGAGACATTAAGAGATGGAGTGGTCTTTGGTGCCAGCCCTATTCC	1511	
QY	760	TGCTGCTTTTCAATTGACAGTATTACGATTTGTGAGCGTAAACAGCCCTACATTCCTTTGGCC	819	
DB	1510	TGCTGCTTTTCAATTGACAGTATTACGATTTGTGAGCGTAAACAGCCCTACATTCCTTTGGCC	1451	
QY	820	TGCTCTCTGTGACCATCAGCTTTTAGATATATCAAGGGTGTGATCCAGCTATCCAGAAAT	879	
DB	1450	TGCTCTCTGTGACCATCAGCTTTTAGATATATCAAGGGTGTGATCCAGCTATCCAGAAAT	1391	
QY	880	CAGATGAGGCCACCCATTCAGGCGCATATCTGGATCTGAAGTTGCTATATCTGAGGAGT	939	
DB	1390	CAGATGAGGCCACCCATTCAGGCGCATATCTGGATCTGAAGTTGCTATATCTGAGGAGT	1331	
QY	940	TGGTTTCAGAACTACAGTAATTTCTGCTCTTGGTCTAGTGAACTGCACAGATAAGAACTCA	999	
DB	1330	TGGTTTCAGAACTACAGTAATTTCTGCTCTTGGTCTAGTGAACTGCACAGATAAGAACTCA	1271	
QY	1000	GGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTGTGATGGG	1059	

DB	1270	GGCCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTGTGATGGG	1211	
QY	1060	TATTTACCTATGTTGGTGCCCTTTTAATAGTCTTGACACTACTACTGATTTTGGCTCTCATTT	1119	
DB	1210	TATTTACCTATGTTGGTGCCCTTTTAATAGTCTTGACACTACTACTGATTTTGGCTCTCATTT	1151	
QY	1120	CATCTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCAACAGATAGATCATTTATCTAG	1179	
DB	1150	CATCTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCAACAGATAGATCATTTATCTAG	1091	
QY	1180	GACTTGCATAAAGAAATGTTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATCCCTGAT	1239	
DB	1090	GACTTGCATAAAGAAATGTTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATCCCTGAT	1031	
QY	1240	TGAAGCGCAAGCTGAATGAAACCGCCCAAAATTAATTTAGTAGGAGTTTCATCTTTTAAAGGG	1299	
DB	1030	TGAAGCGCAAGCTGAATGAAACCGCCCAAAATTAATTTAGTAGGAGTTTCATCTTTTAAAGGG	971	
QY	1300	GATATTCATTTGATTTATACGGGGGAGGCTCAGGGAAGAACGAACTTGACGTTCAGTGC	1359	
DB	970	GATATTCATTTGATTTATACGGGGGAGGCTCAGGGAAGAACGAACTTGACGTTCAGTGC	911	
QY	1360	AGTTTTCACAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACTGCTTGTGAGGAAAAAT	1419	
DB	910	AGTTTTCACAGATCGTTGTTAGATCTTTTATTTTATAGCCATGCACTGCTTGTGAGGAAAAAT	851	
QY	1420	ACCTGTCTTGACTGCCATGTTTCATCATCTTAAAGTATTGTAAGCTGCTATGTATGGAAT	1479	
DB	850	ACCTGTCTTGACTGCCATGTTTCATCATCTTAAAGTATTGTAAGCTGCTATGTATGGAAT	791	
QY	1480	TAAACCGTAAATCATATCTTTTCTCTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATAT	1539	
DB	790	TAAACCGTAAATCATATCTTTTCTCTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATAT	731	
QY	1540	TTTACTTTTGTGACAGATGCTTTCGCCGATCTTGGCAAGTTGACAGAGTGTGGAGCTAG	1599	
DB	730	TTTACTTTTGTGACAGATGCTTTCGCCGATCTTGGCAAGTTGACAGAGTGTGGAGCTAG	671	
QY	1600	AAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1659	
DB	670	AAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	611	
QY	1660	GCAGATTTTCTGAAATGAAATGTTTGTGTAACGAGATCATACCGGTAAGACAGAGAAATGA	1719	
DB	610	GCAGATTTTCTGAAATGAAATGTTTGTGTAACGAGATCATACCGGTAAGACAGAGAAATGA	551	
QY	1720	CAAAAGCTTGTCTTCTGGTATGTTCTAGGCTGATTTGACACTTTTACTGTTATATTAATG	1779	
DB	550	CAAAAGCTTGTCTTCTGGTATGTTCTAGGCTGATTTGACACTTTTACTGTTATATTAATG	491	
QY	1780	CCAATAAGTAAATATAGATTAATATGTAAGTGTGTTTCAAAAGCTTTAGACCTTTTACC	1839	
DB	490	CCAATAAGTAAATATAGATTAATATGTAAGTGTGTTTCAAAAGCTTTAGACCTTTTACC	431	
QY	1840	TTCCAGCCACCCACAGTGTGATTTTTCAGAGTCAGTCAATGGTTATATACATGTGTAGT	1899	
DB	430	TTCCAGCCACCCACAGTGTGATTTTTCAGAGTCAGTCAATGGTTATATACATGTGTAGT	371	
QY	1900	TCCAAAGCACAATAAGCTAGAAAGAAATATTTCTAGGAGCACTACCACTCTGTTTTCAC	1959	
DB	370	TCCAAAGCACAATAAGCTAGAAAGAAATATTTCTAGGAGCACTACCACTCTGTTTTCAC	311	
QY	1960	ATGAAATGCCACACATAGAACTCCAAACATCAATTTTCAATTTGACAGAGTCACTGTA	2019	
DB	310	ATGAAATGCCACACATAGAACTCCAAACATCAATTTTCAATTTGACAGAGTCACTGTA	254	
QY	2020	GTTAAATTTGTTCACAGAACTATGCACTGAACTTAATGCTTCCAAAAATGTTGTTGTTT	2079	
DB	253	GTTAAATTTGTTCACAGAACTATGCACTGAACTTAATGCTTCCAAAAATGTTGTTGTTT	194	
QY	2080	GCAATATCAAAACATTTGTTGCAAGAAATTTAATTAACAAATGAGATTTATACCAT	2139	
DB	193	GCAATATCAAAACATTTGTTGCAAGAAATTTAATTAACAAATGAGATTTATACCAT	134	

Qy	2140	TGCGTTTAAGCTGTACTGAACCTAAATCTGTGGGAATGCATTTGTGAACCTGTAAAGCAAG	2199
Db	133	TGCGTTTAAGCTGTACTGAACCTAAATCTGTGGGAATGCATTTGTGAACCTGTAAAGCAAG	74
Qy	2200	TATCAATAAAGCTTATAGACTTAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	2240
Db	73	TATCAATAAAGCTTATAGACTTAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	33

RESULT 8

ADI62860
ID ADI62860 standard; cDNA; 1599 BP.

AA
AC ADI62860;

DT 22-APR-2004 (first entry)

Human apoptosis-associated cDNA SEQ ID 303.

apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
antirheumatic; antiarthritic; dermatological; antiinflammatory;
hepatotropic; virucide; nootropic; anticoagulant; antiparkinsonian;
vasotrophic; cerebroprotective; antialcoholic; gene therapy; tumour;
antitumourne disease; degenerative disease; viral infection; leukaemia;
carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
lupus; hepatitis; influenza viruses; Alzheimer's disease;
Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
alcoholic liver disease; human; gene; ss.

XX Homo sapiens.

XX PN WO2003058021-A2.

XX
PD 17-JUL-2003.

13-JAN-2003: 2003WO-EP0000270

11-JAN-2002: 2002DE-01000856.

PA (XANT-) XANTOS BIOMEDICINE AG.

PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;

WPI: 2003-542134/51.

PT New nucleic acids involved in apoptosis, useful for diagnosis and
PT treatment of e.g. tumors and degenerative disease, also related proteins,
PT antibodies and modulators.

PS Claim 1b: SEQ ID NO 303: 517bp; German.

This invention describes novel nucleic acid molecules that are associated with apoptosis and encode a polypeptide and are derived from a normalised gene library (embryonic or liver) or clone collections, and the extent of apoptosis measured by cell death detection assay or the CPRG assay (measuring loss of membrane integrity). The products of the invention have cytostatic, neuroprotective, immunosuppressive, anti-rheumatic, antiarthritic, dermatological, anti-inflammatory, hepatotropic, virucide, antiapoptotic, anticonvulsant, antiparkinsonian, vasodilatory, cerebroprotective and antialcoholic activity and can be used for gene therapy. The polynucleotides also related vectors, hosts (or their extracts), encoded polypeptide (or their receptors) and/or agents that inhibit their activity (including antisense sequences) are used for treatment or prevention of tumours, autoimmune or degenerative diseases and viral infections, specifically leukaemia, carcinoma, sarcoma, multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection with hepatitis or influenza viruses, Alzheimer's, Huntington's or Parkinson's diseases, reperfusion injury, stroke and alcoholic liver disease. Detection of the polynucleotides and derived polypeptides can also be used for diagnosis of these diseases. This sequence encodes an apoptosis-associated protein described in the disclosure of the invention.

Db 961 CACGATAAAGGAACCTACGGCGCCTCTTCTTAGTGTGATTTAGTGTGATTTCTCTGAAAGTT 1020
Qy 1043 TGCAGTGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGTCTGACACTACT 1102
Db 1021 TGCAGTGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGTCTGACACTACT 1080
Qy 1103 GATTTTGGCTCTCATTTTCACCTTTCAGTGTCTCTTATTTATGAACGGCATCAGGCACA 1162
Db 1081 GATTTTGGCTCTCATTTTCACCTTTCAGTGTCTCTTATTTATGAACGGCATCAGGCACA 1140
Qy 1163 GATAGATCATTTATCTAGGACTTGCAAAATGAAGTGTAAAGTGTATGCTTAAATATCCA 1222
Db 1141 GATAGATCATTTATCTAGGACTTGCAAAATGAAGTGTAAAGTGTATGCTTAAATATCCA 1200
Qy 1223 AGCAAAATCCCTGATTTCAAGCGCAAGCTGAAATGAAGAAAGCCCAAAATTAATTAGTAGG 1282
Db 1201 AGCAAAATCCCTGATTTGAAGCGCAAGCTGAAATGAAGAAAGCCCAAAATTAATTAGTAGG 1260
Qy 1283 AGTTCATCTTTAAAGGGATATTCATTTGATTTATACGGGGAGGGTCAAGGAAGAACGAA 1342
Db 1261 AGTTCATCTTTAAAGGGATATTCATTTGATTTATACGGGGAGGGTCAAGGAAGAACGAA 1320
Qy 1343 CCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTAGATCTTTATTTTAGCCATGCAC 1402
Db 1321 CCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTAGATCTTTATTTTAGCCATGCAC 1380
Qy 1403 TGTTGTGAGGAAAAATACCTGTCTTGACTGTCATGTCATCATCTTTAAAGTATTGTA 1462
Db 1381 TGTTGTGAGGAAAAATACCTGTCTTGACTGTCATGTCATCATCTTTAAAGTATTGTA 1440
Qy 1463 GCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTTC-----CTATCTGAGGCACCTGG 1518
Db 1441 GCTGCTATGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGG 1500
Qy 1519 TGGATAAATAAACCTGTATATTTTACTTGTTCAGATAGTCTTGCCGCATCTTGGCAAG 1578
Db 1501 TGGATAAATAAACCTGTATATTTTACTTGTTCAGATAGTCTTGCCGCATCTTGGCAAG 1560
Qy 1579 TTGCAGAGATGGTGAGCTAGAAAAAAGAAAAA 1615
Db 1561 TTGCAGAGATGGTGAGCTAGAAAAAAGAAAAA 1597
RESULT 9
ID ADR83534
XX ADR83534 standard; DNA; 4789 BP.
XX
AC ADR83534;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human reticulon 4 DNA, target gene of miRNA.
XX
KW human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;
KW siRNA silencing precursor; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antiinflammatory; immunotherapy; reticulon 4.
XX
OS Homo sapiens.
XX
PN WO2004076622-A2.
XX
PD 10-SEP-2004.
XX
PF 10-FEB-2004; 2004WO-JP001433.
XX
PR 10-FEB-2003; 2003US-0445829P.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI Taira K, Kawasaki H;
XX

DR WPI; 2004-653393/63.
XX
PT Modulating expression of a target gene in a cell, for treating cancer, an
PT immune disease, or a nerve disorder, comprises introducing into the cell
PT a polynucleotide that forms a duplex region with an mRNA transcribed from
PT the target gene.
XX
PS Claim 9; SEQ ID NO 436; 865pp; English.
XX
CC This invention relates to a novel method for modulating the expression of
CC a target gene in a cell. Specifically, it refers to the introduction into
CC a cell of a polynucleotide that forms a duplex region with an mRNA
CC transcribed from the target gene, where the duplex region comprises a
CC mammalian mRNA target region i.e. a non-coding microRNA (miRNA) that
CC regulates mRNA at a post-transcriptional level. The present invention
CC describes a method for controlling ontogenesis of a mammal, function of a
CC mammalian cell, differentiation of a mammalian cell or viability of a
CC mammalian cell in the post-transcriptional phase, which comprises
CC introducing a plasmid vector comprising a promoter and nucleic acid
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.
CC Accordingly, it provides a cell therapy method for treating cancer,
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
CC by introducing into the cell the miRNA, siRNA silencing precursor to the
CC miRNA or the plasmid vector. As such, they can be developed into
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,
CC neurotropic, neuroprotective and antiinflammatory activities and hence can
CC be used for immunotherapy. This polynucleotide sequence is a human target
CC gene whose expression is modulated by miRNAs of the invention.
XX
SQ Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;
Query Match 68.4%; Score 1533; DB 13; Length 4789;
Best Local Similarity 100.0%; Pred. No. 1.1e-309;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 693 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAAGACTGGAGTGGTGTGGTGGCCAGC 752
Db 3257 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAAGACTGGAGTGGTGTGGTGGCCAGC 3316
Qy 753 CTATTCCTGCTGCTTTCATTGACAGATTTACAGCATTTGAGCGTTAAGCGCTACATTGCC 812
Db 3317 CTATTCCTGCTGCTTTCATTGACAGATTTACAGCATTTGAGCGTTAAGCGCTACATTGCC 3376
Qy 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 872
Db 3377 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 3436
Qy 873 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 932
Db 3437 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 3496
Qy 933 GAGAGTTGTTTCAAGAAGTACAGTAATTCGCTCTTGGTCTATGTGAAGTGCACGATAAAG 992
Db 3497 GAGAGTTGTTTCAAGAAGTACAGTAATTCGCTCTTGGTCTATGTGAAGTGCACGATAAAG 3556
Qy 993 GAACCTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 1052
Db 3557 GAACCTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 3616
Qy 1053 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACTACTGATTTGGCT 1112
Db 3617 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACTACTGATTTGGCT 3676
Qy 1113 CTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172
Db 3677 CTCAATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 3736
Qy 1173 TATCTAGGACTTGCATAAAGATGTTAAAGATCCTATGGCTAAATCCAAAGCAAAATC 1232
Db 3737 TATCTAGGACTTGCATAAAGATGTTAAAGATCCTATGGCTAAATCCAAAGCAAAATC 3796
Qy 1233 CCTGGATTGAAGCGCAAAAGCTGAATGAAACGCCCAAAATTAATTAGTAGGAGTTCACTT 1292

```
Db 3797 CCTGGATTGAACGCGAAGCTGAATGAACGCCCAAAATATTTAGTAGAGTTTCATCTT 3856
Qy 1293 TAAAGGGGATATTCATTGTGATTATACGGGGGAGGTCAGGGAACGAAACCTTGACGTT 1352
Db 3857 TAAAGGGGATATTCATTGTGATTATACGGGGGAGGTCAGGGAACGAAACCTTGACGTT 3916
Qy 1353 GCAGTGAGGTTTACAGATCGTTGTAGATCTTTATTTTAGCCATGCACGCTTGTGAGG 1412
Db 3917 GCAGTGAGGTTTACAGATCGTTGTAGATCTTTATTTTAGCCATGCACGCTTGTGAGG 3976
Qy 1413 AAAAATTTACCTGTCTGACTGCCATGTGTTTCATCATCTTAAGTATTTGAAGCTGCTATGT 1472
Db 3977 AAAAATTTACCTGTCTGACTGCCATGTGTTTCATCATCTTAAGTATTTGAAGCTGCTATGT 4036
Qy 1473 ATGGATTAAACCGTAATCATATCTTTTCTCTATCTGAGGCACCTGGTGAATAAAAAACC 1532
Db 4037 ATGGATTAAACCGTAATCATATCTTTTCTCTATCTGAGGCACCTGGTGAATAAAAAACC 4096
Qy 1533 TGTATATTTTACTTTTGTGAGATAGTCTTGGCCCATCTTGGCAAGTTGCAGAGATGGTG 1592
Db 4097 TGTATATTTTACTTTTGTGAGATAGTCTTGGCCCATCTTGGCAAGTTGCAGAGATGGTG 4156
Qy 1593 GAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1652
Db 4157 GAGCTAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4216
Qy 1653 GATTGATGAGATTTTCTGAATGAATTTTGTGTTAGACGAGATCATACCGGTAAAGCA 1712
Db 4217 GATTGATGAGATTTTCTGAATGAATTTTGTGTTAGACGAGATCATACCGGTAAAGCA 4276
Qy 1713 GGAATGACAAAGCTGCTTTTCTGGTATGTTCTAGGTGATATGAGTCTTTTCTGTTTATA 1772
Db 4277 GGAATGACAAAGCTGCTTTTCTGGTATGTTCTAGGTGATATGAGTCTTTTCTGTTTATA 4336
Qy 1773 TTAATGCCAATATAAGTAATAGATATATATATATATATATATATATATATATATATAT 1832
Db 4337 TTAATGCCAATATAAGTAATAGATATATATATATATATATATATATATATATATATAT 4396
Qy 1833 CTTTACCTTCCAGCCACCCACAGTGTCTGATATTTTCAGAGTCAAGTCAATTTGTTTATACAT 1892
Db 4397 CTTTACCTTCCAGCCACCCACAGTGTCTGATATTTTCAGAGTCAAGTCAATTTGTTTATACAT 4456
Qy 1893 GTGTAGTTTCCAAAGCACAATAGCTAGAGAAATATTTTCTAGGAGCACTACCATCTGT 1952
Db 4457 GTGTAGTTTCCAAAGCACAATAGCTAGAGAAATATTTTCTAGGAGCACTACCATCTGT 4516
Qy 1953 TTTTCAACATGAAATGCCACACATAGACCTCCCAACACATCAATTTTCAATTTGCAAGACT 2012
Db 4517 TTTTCAACATGAAATGCCACACATAGACCTCCCAACACATCAATTTTCAATTTGCAAGACT 4576
Qy 2013 GACTGTAGTTTAAATTTTGTTCAGAGATCTATGAGTCAATCTAATGCTTCCAAAAATGTTG 2072
Db 4577 GACTGTAGTTTAAATTTTGTTCAGAGATCTATGAGTCAATCTAATGCTTCCAAAAATGTTG 4636
Qy 2073 TTTGTTTGCAAATATCAAAACATTTGTTATGCAAGAAATTTATTAATTAATAAATGAAGATT 2132
Db 4637 TTTGTTTGCAAATATCAAAACATTTGTTATGCAAGAAATTTATTAATTAATAAATGAAGATT 4696
Qy 2133 ATACCATTTGTTTAAAGCTGTACTGAACTTAAATCTGTGGNATCCATTTGTAAGTGTAAA 2192
Db 4697 ATACCATTTGTTTAAAGCTGTACTGAACTTAAATCTGTGGNATCCATTTGTAAGTGTAAA 4756
Qy 2193 AGCAAGTATCAATAAAGCTTATAGACTTAAA 2225
Db 4757 AGCAAGTATCAATAAAGCTTATAGACTTAAA 4789
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RESULT 10

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

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XX 27-NOV-2002 (first entry)
DT Human bone remodelling gene #106.
XX Bone remodelling; osteoporosis; human; gene; ss.
XX Homo sapiens.
XX US6426186-B1.
XX 30-JUL-2002.
XX 18-JAN-2000; 2000US-00484970.
PF 18-JAN-2000; 2000US-00484970.
XX (INCY-) INCYTE GENOMICS INC.
XX Jones KA, Volkmut W, Walker MG;
XX WPI; 2002-673014/72.
XX A combination of polynucleotides which are co-expressed with genes known
PT to be involved in bone remodeling and osteoporosis are useful in an array
PT for the diagnosis of bone remodeling and osteoporosis associated
PT disorders.
XX Claim 1; Col 283-288; 206pp; English.
XX The invention relates to a combination comprising a number of
CC substantially purified and isolated polynucleotides which are co-
CC expressed with genes known to be involved in bone remodeling and
CC osteoporosis. The invention is used to diagnose disorders associated with
CC bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone
CC remodelling genes of the invention
XX
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;
Query Match 68.1%; Score 1525.2; DB 6; Length 4822;
Best Local Similarity 99.3%; Pred. No. 4.6e-308;
Matches 1539; Conservative 0; Mismatches 9; Indels 2; Gaps 1;
Qy 693 GTTGTGACCTCTGTACTGAGAGACATTAAGAGACTGGAGTGTGTTGTGTCGACG 752
Db 3268 GTTGTGACCTCTGTACTGAGAGACATTAAGAGACTGGAGTGTGTTGTGTCGACG 3327
Qy 753 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCCGTAACAGCCTACATTGCC 812
Db 3328 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCCGTAACAGCCTACATTGCC 3387
Qy 813 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 872
Db 3388 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 3447
Qy 873 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGAAATCTGAAGTTGCTATATCT 932
Db 3448 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGAAATCTGAAGTTGCTATATCT 3507
Qy 933 GAGAGTTGGTTTCAAGAGTACAGTAATCTGCTTGGTCACTGTAAGTCCACGATTAAG 992
Db 3508 GAGAGTTGGTTTCAAGAGTACAGTAATCTGCTTGGTCACTGTAAGTCCACGATTAAG 3567
Qy 993 GAACTCAGGCGCTCTCTTGTAGTATGATTTAGTTGATTTCTCTGAAAGTTTGAGTGTG 1052
Db 3568 GAACTCAGGCGCTCTCTTGTAGTATGATTTAGTTGATTTCTCTGAAAGTTTGAGTGTG 3627
Qy 1053 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 1112
Db 3628 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 3687
Qy 1113 CTCAATTTCACTCTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATGATCAT 1172
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Query Match	66.5%	Score 1488.8	DB 6	Length 1798	
Best Local Similarity	99.1%	Pred. No. 1.3e-300			
Matches 1540	Conservative 0	Mismatches 7	Indels 7	Gaps 4	
Qy	692	GGTGTGTTGACCTCTCTGTACTGGAGAGACATTAAAGACACTGGAGCTGGTGTGTTGGTGGCCAG	751		
Db	247	GGTGTGTTGACCTCTCTGTACTGGAGAGACATTAAAGACACTGGAGCTGGTGTGTTGGTGGCCAG	306		
Qy	752	CCTATTCTCTGCTGCTTTTCATTGACAGTAATTCAGCATTTGTGAGCGTAAACAGCCTACATTCG	811		
Db	307	CCTATTCTCTGCTGCTTTTCATTGACAGTAATTCAGCATTTGTGAGCGTAAACAGCCTACATTCG	366		
Qy	812	CTTGGCCCTGCTCTCTGTGTGACATCAGCTTTAGATATACAGGGTGTGATCCAGATAT	871		
Db	367	CTTGGCCCTGCTCTCTGTGTGACATCAGCTTTAGATATACAGGGTGTGATCCAGATAT	426		
Qy	872	CCAGAAATCAGATGAAGGCCACCAATTCAGGGCATATCTGGAATCTCAAGTTGCTATATC	931		
Db	427	CCAGAAATCAGATGAAGGCCACCAATTCAGGGCATATCTGGAATCTCAAGTTGCTATATC	486		
Qy	932	TGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTGAATTCGACGATAA	991		
Db	487	TGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTGAATTCGACGATAA	546		
Qy	992	GGAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTGT	1051		
Db	547	GGAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTTGCAAGTGT	606		
Qy	1052	GATGTGGGTATTTACCTATGTTGGTGCTTGTTTAAATGGTCTGACACTACTGATTTTGGC	1111		
Db	607	GATGTGGGTATTTACCTATGTTGGTGCTTGTTTAAATGGTCTGACACTACTGATTTTGGC	666		
Qy	1112	TCTCATTTTCACT - CTTTCAGTGTTCCTGTATTTATGAAACGGCATCAGGCACAGATAGATC	1170		
Db	667	TCTCATTTTCACTCCTTCAGTGTTCCTGTATTTA - GAAACGGCATCAGGCACAGATAGATC	725		
Qy	1171	ATTATCTAGGACTTGCATAATGAAGATGTTTAAAGATGCTATGGCTTAAATTCACAGCAAAA	1230		
Db	726	ATTATCTAGGACTTGCATAATGAAGATGTTTAAAGATGCTATGGCTTAAATTCACAGCAAAA	785		
Qy	1231	TCCTGTGATTTGAAGCGCAAGCTGAATGAAACCGCCAAATATTTAGTAGGAGTTCATC	1290		
Db	786	TCCTGTGATTTGAAGCGCAAGCTGAATGAAACCGCCAAATATTTAGTAGGAGTTCATC	845		
Qy	1291	TTTAAAGGGATATTCATTTGATTATACGGGGAGGCTCAGGGAAGAACCAACCTTCACG	1350		
Db	846	TTTAAAGGGATATTCATTTGATTATACGGGGAGGCTCAGGGAAGAACCAACCTTCACG	905		
Qy	1351	TTGCAGTGCAGTTTTCACAGATCGTTGTAGATCTTTTATTTTAAAGCATCTGTTGTGA	1410		
Db	906	TTGCAGTGCAGTTTTCACAGATCGTTGTAGATCTTTTATTTTAAAGCATCTGTTGTGA	965		
Qy	1411	GGAAAAATTACCTGCTTTGACTGCCATGTTTTCATCATCTTTAAGTATTTGAAGCTGCTAT	1470		
Db	966	GGAAAAATTACCTGCTTTGACTGCCATGTTTTCATCATCTTTAAGTATTTGAAGCTGCTAT	1025		
Qy	1471	GTATGGATTTAAACCGTAATCATATCTTTTTC - - - CTATCTGAGGCACCTGGTGGAAATAA	1526		
Db	1026	GTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACCTGGTGGAAATAA	1085		
Qy	1527	AAAACTGTATATTTTACTTTTGTGAGATAGTCTTCGCCCATCTTGGCAAGTTGCAGAG	1586		
Db	1086	AAAACTGTATATTTTACTTTTGTGAGATAGTCTTCGCCCATCTTGGCAAGTTGCAGAG	1145		
Qy	1587	ATGTTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTC	1646		
Db	1146	ATGTTGGAGCTAGAAAAAAGAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTC	1205		
Qy	1647	CGTGTAGATTGATCAGATTTTCTGAAATGAAATGTTTGTGTTTGTAGCAGATCATACCGGT	1706		
Db	1206	CGTGTAGATTGATCAGATTTTCTGAAATGAAATGTTTGTGTTTGTAGCAGATCATACCGGT	1265		
Qy	1707	AAAGCAGGAATGACAAAGCTTGTCTTTTCTGTGTATGTTCTAGGTGTATGTGACTTTTACT	1766		

PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.

PS Claim 1; Page 173; 339pp; English.

XX The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them. Also
CC included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the polynucleotides,
CC antibodies that bind to the proteins and identification of modulators of
CC the proteins or the expression of the polynucleotide. The polynucleotides
CC can be used as probes for the identification and isolation of full length
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
CC as nutritional supplements. The protein is useful in the treatment of
CC various immune deficiencies and disorders such as viral infections,
CC bacterial infections, fungal infections, autoimmune disorders (e.g.
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
CC tumours. They are also useful for tissue regeneration, for wound healing
CC and in the treatment of burns, incisions and ulcers. The proteins are
CC also useful for regulating haematopoiesis, for treating myeloid or
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
CC sequences encoding a secreted protein

XX Sequence 1514 BP; 455 A; 258 G; 313 G; 488 T; 0 U; 0 Other;

Query Match 65.8%; Score 1473.4; DB 6; Length 1514;
Best Local Similarity 99.1%; Pred. No. 2e-297;
Matches 1504; Conservative 0; Mismatches 6; Indels 7; Gaps 2;

QY	724	AGAAGACTGGAGTGTGTTGGTGGCAGCCTATTCTCGTCTGCTTTCATTGACGATTCA	783
DB	1	AGAAGACTGGAGTGTGTTGGTGGCAGCCTATTCTCGTCTGCTTTCATTGACGATTCA	60
QY	784	GCATTGTGAGGTACAGCTACATTGCTGGCCCTGCTCTCTGTGACCATCAGCTTTA	843
DB	61	GCATTGTGAGGTAAACGCTTACATTGCTGGCCCTGCTCTCTGTGACCATCAGCTTTA	120
QY	844	GGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGG	903
DB	121	GGATATACAAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGG	180
QY	904	CATATCTGGAATCTGAAGTGTGATATCTGAGGAGTTGGTTCAGAAATGACGATTAATCTG	963
DB	181	CATATCTGGAATCTGAAGTGTGATATCTGAGGAGTTGGTTCAGAAATGACGATTAATCTG	240
QY	964	CTCTTGGTTCATGTGAACCTGACGATAAAGGAACCTCAGCGGCTCTTCTTAGTGTGATGATT	1023
DB	241	CTCTTGGTTCATGTGAACCTGACGATAAAGGAACCTCAGCGGCTCTTCTTAGTGTGATGATT	300
QY	1024	TAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	1083
DB	301	TAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	360
QY	1084	TTAATGGTCTGACACTAGTATTTGGCTCTCATTTTCACTCTCTAGTGTCTCTGTATTT	1143
DB	361	TTAATGGTCTGACACTAGTATTTGGCTCTCATTTTCACTCTCTAGTGTCTCTGTATTT	420
QY	1144	ATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAAATGAAGATGTTAAAG	1203
DB	421	ATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAAATGAAGATGTTAAAG	480
QY	1204	ATGCTATGGTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAAC	1263
DB	481	ATGCTATGGTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAATGAAAC	540
QY	1264	GCCCAAAATATATAGTAGGAGTTCAATCTTTAAAGGGGATATTCATTGATATACGGGG	1323
DB	541	GCCCAAAATATATAGTAGGAGTTCAATCTTTAAAGGGGATATTCATTGATATACGGGG	600

QY	1324	AGGGTCAGGGAAGAACGAACCTTGACGTTGCGAGTGCAGTTCACAGATCGTTGTTAGATC	1383
DB	601	AGGGTCAGGGAAGAACGAACCTTGACGTTGCGAGTGCAGTTCACAGATCGTTGTTAGATC	660
QY	1384	TTTATTTTACCCATGCACTGTTGTGAGGAAAAATACCTGCTTTGACATGCAATGTGTC	1443
DB	661	TTTATTTTACCCATGCACTGTTGTGAGGAAAAATACCTGCTTTGACATGCAATGTGTC	720
QY	1444	ATCATCTTAAGTATGTGAAGCTGTATGTATGGAATTTAAACCGTAATCATATCTTTTC	1502
DB	721	ATCATCTTAAGTATGTGAAGCTGTATGTATGGAATTTAAACCGTAATCATATCTTTTC	780
QY	1503	---CTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGT	1559
DB	781	TATCTATCTGAGGCACTGGTGGAAATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGT	840
QY	1560	CTTGGCGCATCTTGGCAAGTTGCGAGATGTGGAGCTAGAAAAAAGGCC	1619
DB	841	CTTGGCGCATCTTGGCAAGTTGCGAGATGTGGAGCTAGAAAAAAGGCC	900
QY	1620	TTTTTCAGTTTGTGCACTGTGTATGTCCTGCTGATGATTCAGATTTCTGAAATGAAA	1679
DB	901	TTTTTCAGTTTGTGCACTGTGTATGTCCTGCTGATGATTCAGATTTCTGAAATGAAA	960
QY	1680	TGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTCTGCTGTA	1739
DB	961	TGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTCTGCTGTA	1020
QY	1740	TGTTCTAGGTGTAATGTGACATTTTACTGTTATATTAATGTCATATTAAGTAATATAGA	1799
DB	1021	TGTTCTAGGTGTAATGTGACATTTTACTGTTATATTAATGTCATATTAAGTAATATAGA	1080
QY	1800	TTATATATGATAGTGTGTTTCAAAAGCTTACAGCTTTACCTTCCAGCCACCCACAGTGC	1859
DB	1081	TTATATATGATAGTGTGTTTCAAAAGCTTACAGCTTTACCTTCCAGCCACCCACAGTGC	1140
QY	1860	TTGATATTTTCAGAGTCACTGTTTATACATGTTGTTTCCAAAGCACAATAAGCTAGA	1919
DB	1141	TTGATATTTTCAGAGTCACTGTTTATACATGTTGTTTCCAAAGCACAATAAGCTAGA	1200
QY	1920	AGAGAAATATTTTCAGAGCACTACCAATCTGTTTCAACATGAAATGCCACACATAG	1979
DB	1201	AGAGAAATATTTTCAGAGCACTACCAATCTGTTTCAACATGAAATGCCACACATAG	1260
QY	1980	AACTCCACACACATCAATTTTCATTTGCGACAGACTGACCTGAGTAAATTTTGTACAGATC	2039
DB	1261	AACTC---CAACATCAATTTTCATTTGCGACAGACTGACCTGAGTAAATTTTGTACAGATC	1317
QY	2040	TATGAGCTGAATCTAAATGCTTCCAAATGTTGTTTTCGAAATATCAAAACATTTGTA	2099
DB	1318	TATGAGCTGAATCTAAATGCTTCCAAATGTTGTTTTCGAAATATCAAAACATTTGTA	1377
QY	2100	TGCAAGAAATTTAATTTACAAAATGAAGATTTATACATTTGGTTTAAGCTGACTGA	2159
DB	1378	TGCAAGAAATTTAATTTAATTTAATGAAGATTTATACATTTGGTTTAAGCTGACTGA	1437
QY	2160	ACTAAATCTGGAATGCAATTTGCACTGTAAGGCAAGATATCAATTAAGCTTATAGAC	2219
DB	1438	ACTAAATCTGGAATGCAATTTGCACTGTAAGGCAAGATATCAATTAAGCTTATAGAC	1497
QY	2220	TTAAAAAAGGAAAAA 2236	
DB	1498	GTAAGAAACTTAGAAA 1514	

RESULT 13
AAD08386
ID AAD08386 standard; cDNA; 1683 BP.
XX AAD08386;
XX 09-AUG-2001 (first entry)
DT

XX Human secreted protein-encoding gene 42 cDNA clone HAGT48, SEQ ID NO:52.
DE
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification;
KW ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 830..1192
FT /*tag= a
FT /product= "Human secreted protein precursor"
FT /note= "CDS does not include start codon"
FT /partial
FT 830..898
FT sig_peptide /*tag= b
FT 899..1189
FT mat_peptide /*tag= c
FT /product= "Mature human secreted protein"
XX
XX WO200077022-A1.
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US015136.
XX
XX 11-JUN-1999; 99US-0138629P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-367020/38.
XX P-PSDB; AAE03939.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX disease, botulism, cancers and Scimitar syndrome.
XX
XX Claim 1; Page 520; 614pp; English.
XX
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.
XX The genes and their secreted proteins are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 50 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angiogenic disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
XX Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;
Query Match 65.4%; Score 1464.6; DB 4; Length 1683;
Best Local Similarity 95.6%; Pred. No. 1.4e-295;
Matches 1544; Conservative 1; Mismatches 0; Indels 70; Gaps 1;
Qy 1 CGTCACACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACCC 60
Db 96 CGTCACACAGTAGTCCCTCGGCTCAGTCGGCCAGCCCTCTCAGTCTCTCCCAACCC 155
Qy 61 CCACAAAGCGCCGCGGCTCTGAGACGCGGCCCGCGCGCGCGCGAGCTGCAGCATC 120
Db 156 CCACAAAGCGCCGCGGCTCTGAGACGCGGCCCGCGCGCGCGAGCTGCAGCATC 215
Qy 121 ATCTCCACCTCCAGCCATCGAAGACCTGGAACAGTCTCTCTGTCCTCTCGGACA 180
Db 216 ATCTCCACCTCCAGCCATCGAAGACCTGGAACAGTCTCTCTGTCCTCTCGGACA 275
Qy 181 GCCCAGCCCGCGCGCGGCTTCAAGTACAGATTCCTGAGGAGCGCCGAGGACGAGG 240
Db 276 GCCCAGCCCGCGCGCGGCTTCAAGTACAGATTCCTGAGGAGCGCCGAGGACGAGG 335
Qy 241 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 336 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 395
Qy 301 TGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 396 TGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 455
Qy 361 GCGCGCCCTGATGAGACTTCGGAATGACTTCGTCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 456 GCGCGCCCTGATGAGACTTCGGAATGACTTCGTCGCGCGCGCGCGCGCGCGCGCGCG 515
Qy 421 GCGCGCTCCCG 480
Db 516 GCGCGCTCCCG 575
Qy 481 CGACCGTCCCG 540
Db 576 CGACCGTCCCG 635
Qy 541 AGGACGAGGAGCTTCG 600
Db 636 AGGACGAGGAGCTTCG 695
Qy 601 CAGAGCCCGTGTGAGACCG 660
Db 696 CAGAGCCCGTGTGAGACCG 755
Qy 661 CGCCCAAGCGCAGGCGCTCTCGGGCTCAGTGGTGTGTGAGCTCTCTGTCGAGAGACA 720
Db 756 CGCCCAAGCGCAGGCGCTCTCGGGCTCAGTGGTGTGTGAGCTCTCTGTCGAGAGACA 815
Qy 721 TTAAGAGACTGGAGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 816 TTAAGAGACTGGAGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
Qy 781 TCAGCATGTGAGCGTAACAGCTTACATTGGCTTGGCGCTCTCTCTGTGACCATCAGT 840
Db 876 TCAGCATGTGAGCGTAACAGCTTACATTGGCTTGGCGCTCTCTCTGTGACCATCAGT 935
Qy 841 TTAGATATACAGGGGTGATCCAACTATCCAGAAATCAGATGAAGGCCACCATTCATCA 900
Db 936 TTAGATATACAGGGGTGATCCAACTATCCAGAAATCAGATGAAGGCCACCATTCATCA 995

Db 3574 CTCAATTCACCTCTTCAGTGTTCCTGTTATTTATGACGCAATCAGGCACAGATAGATCAT 3633
Qy 1173 TATCTAGGACTTGCATAAATAAGATGTTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATC 1232
Db 3634 TATCTAGGACTTGCATAAATAAGATGTTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATC 3693
Qy 1233 CCTGGATTGAAGCCCAAGCTGAATGAAGCCCAAGCTGAATGAAGCTGAATGAAGCTGAAT 1292
Db 3694 CCTGGATTGAAGCCCAAGCTGAATGAAGCCCAAGCTGAATGAAGCTGAATGAAGCTGAAT 3753
Qy 1293 TAAAGGGGATATTCATTTGATTTATACAGGGGAGGCTCAGGCAAGCAACCTTGACGTT 1352
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Qy 1653 GATTGATGCAGATTTCTGAAATCAATGTTTGTAGCAGATCATACCGTAAGCA 1712
Db 4054 GATTGATGCAGATTTCTGAAATCAATGTTTGTAGCAGATCATACCGTAAGCA 4113
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Qy 1773 TTAATGCAATATAAGTAATATAGATATATATATATATATATATATATATATATATATATAT 1832
Db 4174 TTAATGCAATATAAGTAATATAGATATATATATATATATATATATATATATATATATATAT 4233
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Db 4234 CTTTACCTTCCAGCCACCCACAGTCTGTATATTTTCACTGCTAGTCACTGTTGTTATACAT 4293
Qy 1893 GTGTAGTTTCCAAAGCACATAAGCTAGAGAGAAATATTTCTAGGAGCACTTACCATCTGT 1952
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Qy 2133 ATACCATTTGTTTAAAGCTGTACTGAACTAAATCTGTGGAAATGCAATTTGGAATGTA 2192
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Db 4594 AGCAAGTATCAATAAGCTTATAGACTTAAAAAATA 4632

RESULT 15
ADG32772
ID ADG32772 standard; DNA; 4632 BP.
XX
AC ADG32772;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human DNA differentially expressed in patients with SLE SeqID96.
XX
KW human; ds; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis.
XX
OS Homo sapiens.
XX
FN W02003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N;
XX
DR WPI; 2003-877243/81.
XX
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.
XX
PS Claim 18; SEQ ID NO 96; 877pp; English.
XX
CC This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This polynucleotide is a DNA sequence representing human mRNA that is
CC differentially expressed in patients with SLE, used in an exemplification
CC of the invention.
XX
SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Query Match 62.9%; Score 1409; DB 10; Length 4632;
Best Local Similarity 96.1%; Pred. No. 8.2e-284;
Matches 1479; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

Qy 693 GTTGTGACCTCTCTACTGAGAGACATTAAGAGACTGGAGTGGTGGTGGCCAGC 752
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Db 3334 CAGAAATCAGATGAAGGCCACCCATTTCAAGGCATATCTGGAACTCTGAAGTTGCTATATCT 3393
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Db 3454 GAACTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 3513
QY 1053 ATGTGGGTATTTTACCTATGTTGGTGCCTTGTAAATGCTCTGACACTACTGATTTTGGCT 1112
Db 3514 ATGTGGGTATTTTACCTATGTTGGTGCCTTGTAAATGCTCTGACACTACTGATTTTGGCT 3573
QY 1113 CTCATTTTCACTCTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCCACAGATGATCAT 1172
Db 3574 CTCATTTTCACTCTTTCAGTGTTCCTGTTATTTATGNAACGGCATCAGGCCACAGATGATCAT 3633
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QY 1233 CCTGGATTTGAAGCGCAAGCTGGAATGAANAACCCCAAAATTAATTAGTAGGAGTTCACTTT 1292
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QY 1293 TAAAGGGGATATTTCATTTTGAATTTATACGGGGGAGGTTCAGGGAAGAACGAACCTTGACGTT 1352
Db 3754 TAAAGGGGATATTTCATTTTGAATTTATACGGGGGATTTAGT----- 3780
QY 1353 GCAGTGCAGTTTTCACAGATCGTTGTTAGATCTTTATTTTATAGCCATGCACCTGTTGTGAGG 1412
Db 3781 -----GATCTTTATTTTATAGCCATGCACCTGTTGTGAGG 3813
QY 1413 AAAAAATTACCTGCTCTGTGATGCCATGCTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 1472
Db 3814 AAAAAATTACCTGCTCTGTGATGCCATGCTTTCATCATCTTAAGTATTGTAAGCTGCTATGT 3873
QY 1473 ATGGATTTAAACCGTAATCATATCTTTTCCCTATCTGAGGCACTGGTGGAAATAAAAAACC 1532
Db 3874 ATGGATTTAAACCGTAATCATATCTTTTCCCTATCTGAGGCACTGGTGGAAATAAAAAACC 3933
QY 1533 TGTATATTTTATCTTTGTTGCAGATAGTCTTGCCGCATCTTGCCAAAGTTGCAGAGATGGTG 1592
Db 3934 TGTATATTTTATCTTTGTTGCAGATAGTCTTGCCGCATCTTGCCAAAGTTGCAGAGATGGTG 3993
QY 1593 GAGCTAGAAAAAATAAAAAAAGCCCTTTTCAGTTTGTGACCTGTGTATGGTCCGTGTA 1652
Db 3994 GAGCTAGAAAAAATAAAAAAAGCCCTTTTCAGTTTGTGACCTGTGTATGGTCCGTGTA 4053
QY 1653 GATTGATCGAGATTTTCTGAAATGAATGAAATGTTTGTAGACGAGATCATCCGTAAGCA 1712
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Db 4354 TTTCAAACATGAAATGCCACACACATAGAACTCCAAACAACATCAATTTTCATTGCAAGACT 4413
QY 2013 GACTGTAGTTTAAATTTTGTCAAGAACTCTATGGACTGAAATCTAAATGCTTCCAAAAATGTTG 2072
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Db 4594 AGCAAAAGTATCAATAAAAGCTTTATAGACTTAAAAAATAAAAA 4632

Search completed: August 1, 2005, 15:32:35
Job time : 1124 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2005, 13:22:45 ; Search time 6519 Seconds
(without alignments)
13079.301 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 69479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gesi.*
9: gb_gesi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1488.8	66.5	1798	3 AF125103	AF125103 Homo sapi
2	1359.2	60.7	1785	3 AF077050	AF077050 Homo sapi
3	1355	60.5	1540	3 CR611869	CR611869 full-leng
4	1035.4	46.2	3533	3 AK034902	AK034902 Mus muscu
5	957.4	42.7	1097	5 BX439214	BX439214 BX439214
c 6	917.2	40.9	1028	5 BX426504	BX426504 BX426504
7	885	39.5	1003	4 BM469019	BM469019 AGNCOURT
8	881.2	39.3	911	1 AL549191	AL549191 AL549191
9	861.2	38.4	875	1 AL573494	AL573494 AL573494
10	844.6	37.7	1008	4 BM450461	BM450461 AGNCOURT
11	844.2	37.7	1003	3 CK231727	CK231727 ILLUMIGEN
12	837.2	37.4	901	5 BQ879359	BQ879359 AGNCOURT
13	831.8	37.1	1164	7 CK232009	CK232009 ILLUMIGEN
14	831	37.1	956	7 CN644030	CN644030 ILLUMIGEN
15	819.2	36.6	1031	7 CN647521	CN647521 ILLUMIGEN
16	815.6	36.4	987	7 CO647477	CO647477 ILLUMIGEN
c 17	803.4	35.9	982	1 AL526343	AL526343 AL526343
18	799.4	35.7	916	7 CN644991	CN644991 ILLUMIGEN
19	797.6	35.6	910	5 BQ959498	BQ959498 AGNCOURT
c 20	781.4	34.9	783	5 BQ001312	BQ001312 UI-H-DH1-
21	779.8	34.8	1002	5 BX462171	BX462171 BX462171
22	779.6	34.8	1022	4 BM557554	BM557554 AGNCOURT
23	776.2	34.7	983	7 CN803408	CN803408 ILLUMIGEN
c 24	775	34.6	787	5 BQ774392	BQ774392 UI-H-EZ1-

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26	771.8	34.5	1008	7	CN801982	CN801982	ILLUMIGEN
27	771.6	34.4	882	5	BX426505	BX426505	ILLUMIGEN
28	771.4	34.4	920	7	CN644247	CN644247	ILLUMIGEN
c 29	770.8	34.4	775	6	CA308369	UI-H-FT1-	ILLUMIGEN
c 30	770.8	34.4	812	6	CD370277	UI-H-FT1-	ILLUMIGEN
c 31	770.2	34.4	960	7	CN646472	ILLUMIGEN	ILLUMIGEN
c 32	769.8	34.4	936	2	BF570468	BF570468	602186269
c 33	767.4	34.3	789	5	BUE19407	UI-H-FT1-	ILLUMIGEN
c 34	764.6	34.1	986	7	CN801944	CN801944	ILLUMIGEN
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c 36	761.2	34.0	800	7	CN429706	170005999	ILLUMIGEN
c 37	760.4	33.9	784	6	CA308887	UI-H-FT1-	ILLUMIGEN
38	759.4	33.9	1020	7	CN643337	ILLUMIGEN	ILLUMIGEN
39	753.8	33.7	882	5	BQ233389	BQ233389	AGNCOURT
c 40	750.2	33.5	781	6	CD368020	UI-H-FT1-	ILLUMIGEN
c 41	747.2	33.4	754	6	CD367884	UI-H-FT1-	ILLUMIGEN
c 42	744	33.2	799	6	CA312856	UI-CF-FN0	ILLUMIGEN
c 43	743	33.2	785	6	CA310107	UI-H-FT1-	ILLUMIGEN
c 44	740.4	33.1	783	5	BUE26517	UI-H-FT0-	ILLUMIGEN
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ALIGNMENTS

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LOCUS Homo sapiens neuroendocrine specific protein c homolog mRNA,
DEFINITION complete cds.
ACCESSION AF125103
VERSION AF125103.1 GI:5107001
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G.,
Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
Genome Res. 10 (10), 1546-1560 (2000)
JOURNAL 20499367
MEDLINE 11042152
PUBMED 2 (bases 1 to 1798)
AUTHORS Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.
TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1798)
AUTHORS Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,
Dai, M., Huang, Q., Chen, S. and Chen, Z.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China
FEATURES
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Qy	692	GGTTGTTTGACCTCTCTGCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTTCGGTGCCAG	751
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Qy	752	CCATTCCTGCTGCTTTTCATGTGACAGPATTCAGCATTTGAGCGGTAAACAGCCCTACATTGC	811
Db	307	CCATTCCTGCTGCTTTTCATGTGACAGPATTCAGCATTTGAGCGGTAAACAGCCCTACATTGC	366
Qy	812	CTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAACTAT	871
Db	367	CTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAACTAT	426
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Qy	992	GGAACTCAGGGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGTGTT	1051
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Qy	1112	TCTCATTTCACT -CTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATC	1170
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ORIGIN
Query Match      60.7%; Score 1359.2; DB 3; Length 1785;
Best Local Similarity 99.1%; Pred. No. 1.7e-288;
Matches 1409; Conservative 0; Mismatches 8; Indels 5; Gaps 4;

Qy 692 GGTGTTGACCTCTCTGCTGACGAGACATTAAAGAGACTGAGTGTGTTGGTGCCAG 751
Db |||
Qy 246 GGTGTTGACCTCTCTGCTGACGAGACATTAAAGAGACTGAGTGTGTTGGTGCCAG 305
Db |||
Qy 752 CCTATTCTGCTGCTCTCAATGACAGTATTGAGCATTGTGAGCGTAACAGCTACATTGC 811
Db |||
Qy 306 CCTATTCTGCTGCTCTCAATGACAGTATTGAGCATTGTGAGCGTAACAGCTACATTGC 365
Db |||
Qy 812 CTGCGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 871
Db |||
Qy 366 CTGCGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 425
Db |||
Qy 872 CCAGAAATCAGATGAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATC 931
Db |||
Qy 426 CCAGAAATCAGATGAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATC 485
Db |||
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Db |||
Qy 486 TGAGGAGTTGTTTCCAGAAATGACAGTAAATCTGCTCTTGGTCAATGAGTGCAGATAAA 545
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Db |||
Qy 606 GATGCGGTATTTACCTATGTTGCTGCTGTTTAAATGCTGACACTGACTGTTTGGC 665
Db |||
Qy 1112 TCTCAATTCACCTCTTCTGAGTGTCTGTTTATTAAGACGGCATCAGGCACAGATAGATCA 1171
Db |||
Qy 666 TCTCAATTCACCTCTTCTGAGTGTCTGTTTATTAAGACGGCATCAGGCACAGATAGATCA 725
Db |||
Qy 1172 TTATCTAGGACTTCAATAAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 1231
Db |||
Qy 726 TTATCTAGGACTTCAATAAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 785
Db |||
Qy 1232 CCCTGGATTGAAGCGCAAGCTGAATGAAACGCCCAAAATTAATAGTAGGAGTTTCATCT 1291
Db |||
Qy 786 CCCTGGATTGAAGCGCAAGCTGAATGAAACGCCCAAAATTAATAGTAGGAGTTTCATCT 845
Db |||
Qy 1292 TTAAGGGGATATTCAATTTGATTATACGGGGAGGGTCAGGGAAGAACGAACTTTGACGT 1351
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Qy 846 TTAAGGGGATATTCAATTTGATTATACGGGGAGGGTCAGGGAAGAACGAACTTTGACGT 905
Db |||
Qy 1352 TGCAGTGCAGTTTACAGATGTTGTTAGATCTTTTATTTTAGCCATGCACTGTTGTGAG 1411
Db |||
Qy 906 TGCAGTGCAGTTTACAGATGTTGTTAGATCTTTTATTTTAGCCATGCACTGTTGTGAG 965
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Qy 1412 GAAAAATTACCTGCTTGCATGCGAATGTTTCATCATCTTAAGTATTGTAAGCTGCTATG 1471
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Qy 1026 TATGATTTAAACCGTAATCATATCTTTTCTCTATCTGAGGCATCTGGTGAATAAAAAAC 1085
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1386 ACCTTTACCTTCCAGCCACCCACAGTCTTGATATTTTCAGAGTCAGTCAITGGTTATAC 1445
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1506 GTTTTCAACATGAAATGCCACACACATAGAACTCCAAACACATCAATTTTCATTGCACAGA 1565
2011 CTGACTGTAGTAAATTTTGTTCACAGAACTATGAGCTGAATCTTAATGCTTCCAAAATGT 2070
1566 CTGACTGTAGTAAATTTTGTTCACAGAACTATGAGCTGAATCTTAATGCTTCCAAAATGT 1623
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1624 TGTTTGT--GCAAAATACCAACATTTGTTATGCAAGAAATTTT 1663

RESULT 3
CR611869 1540 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
(human).
ACCESSION CR611869
VERSION 1 GI:50492676
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1540)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1540)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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ORIGIN

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Query Match          60.5%; Score 1355; DB 3; Length 1540;
Best Local Similarity 99.5%; Pred. No. 1.4e-287;
Matches 1382; Conservative 0; Mismatches 0; Indels 7; Gaps 2;

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QY 812 CTGTGCCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAGCTAT 871
D5 275 CTGTGCCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAGCTAT 334

QY 872 CCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAATCTGAAATCTGATATC 931
D5 335 CCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAATCTGAAATCTGATATC 394

QY 932 TGAGGAGTTGGTTTCAAGAGTACAGTAATCTGCTCTTGGTCACTGTAAGTGTGATGATCA 991
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QY 1768 TTATATAATTGCCAATAATAAGTAAATATAGATTATATATATATATAGTGTGTTTACAAAGCT 1827
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QY 1888 TACATGTGTAGTTTCCAAAGCACAATAAGCTAGAAGAAGAAATATTTTCTAGGAGCACTACCA 1947
D5 1355 TACATGTGTAGTTTCCAAAGCACAATAAGCTAGAAGAAGAAATATTTTCTAGGAGCACTACCA 1414

QY 1948 TCTGTTTTCACATGAATGCCACACACATAGAACTCCAAACATCAATTTTCAATTGTCAC 2007
D5 1415 TCTGTTTTCACATGAATGCCACACACATAGAACTCCAAACATCAATTTTCAATTGTCAC 1471

QY 2008 AGACTGACTGTAGTTAAATTTTGTTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAA 2067
D5 1472 AGACTGACTGTAGTTAAATTTTGTTCACAGAATCTATGGACTGAATCTAATGCTTCCAAAA 1531

QY 2068 TGTGTTTGTG 2076
D5 1532 TGTGTTTGTG 1540

RESULT 4
AK034902
LOCUS
DEFINITION
Mus musculus 12 days embryo mRNA linear HTC 03-APR-2004
and neck cDNA, RIKEN full-length enriched library, clone:9430089L06
product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN)
(FOOCN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus
norvegicus], full insert sequence.
ACCESSION
AK034902
VERSION
AK034902.1 GI:26084268
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
3
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
```


AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

REFERENCE Nature 409, 685-690 (2001)

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

REFERENCE Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 3533)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saigo, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ac.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>

FEATURES

Source

1. 3533

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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1. 3533

/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOCO PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog (Rattus norvegicus) (SWISSPROT|Q9UK11, evidence: FASTA, 95.8%ID, 100%length, match=1068)"

ORIGIN

Query Match 46.2%; Score 1035.4; DB 3; Length 3533;

Best Local Similarity 77.0%; Pred. No. 4.5e-217;

Matches 1710; Conservative 0; Mismatches 341; Indels 170; Gaps 30;

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Db 126 CTTGGTTGGCGCAGCCGGCTCTGCCAGTCTCTGCCNACCCCAACCGCCGCGGCT 185

Qy 79 CTGAGACGCGCCCGCGCGCGGCGGAGCTGCAGATCATCTCCACCTCCAGCCA 138

Db 186 CTGAG--GAGAAGTGGCCGCGCGGCGGAGTAGTGCAGATCAT-----CGCCGACCA 236

Qy 139 TGGAGACCTGACGAGTCTCTCTGGT---CTGCTCTGGACAGCCACCGCCGCGGC 195

Db 237 TGGAGACATGACGAGTCGTCTGGTCTCTCTGTCGCGGATAGCCCGCCGCGGCC 296

Qy 196 AGCCCGGTTCAAGTACCACTTCGTGAGGAGCCCGAGGACGAGGAGAGAGAGAGG 255

Db 297 CGCCCGGTTTCAAGTACCACTTCGTGAGGAGCCCGAGGACGAGGAGAGAGAGAG 356

Qy 256 AGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315

Db 357 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416

Qy 316 CCGCCCGGGCTGTCCGCGGCGCCAGTGCACCGCCCTGCGCGCGCGCGCCCTG 375

Db 417 CAGCGCGGGCTGTCCGCGGCTCCGCTGCC-----CCCGCGCGCGCACCGCTG 467

Qy 376 ACTTCGGAATAGATTCTGTCGCCCGCGCGCCCGGGGAGCCCTGCGCGCGCTC 435

Db 468 ACTTCAGCAGCAGTCTGGTGTCCCGCGCGCGCGCGCGCGCTCCCGCGCGCG 527

Qy 436 TCGCCCGGAGCGGAGCGGCTCTTTGGGACCCGAGCGCGGCTGCTGCAGCGTGC 495

Db 528 CCGCCCTTGAGAGGCGAGCGCTCTCTGGGAACGAGCGCCCGCGCGCT----- 578

Qy 496 CATCCCGCTGTCTGCTGCGCGAGTCTCGCCCTCCCAAGCTCCCTGAGGAGCAG 555

Db 579 CATCCCTGCGCGCGCTGCGCGAGTCTGCTCCCAAGCTCCCGGAGGAGCAGCG 638

Qy 556 CGGCGCGCGCTCCCGCTCTCTCCCGCGCGAGCGTGCAGCGCCCGCGCGTGTG 615

Db 639 CAGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 670

Qy 616 CCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675

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Qy 1096 CACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTTATTAAG 1155

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QY 2222 A 2222
Db 2193 A 2193
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RESULT 5
BX439214
LOCUS
DEFINITION BX439214 Homo sapiens PLACENTA 1097 bp mRNA linear EST 04-MAY-2004
CS0DE008YG04

5-PRIME, mRNA sequence.
BX439214
BX439214.2 GI:47020895
EST.
Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On May 15, 2003 this sequence version replaced gi:30787776.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1423.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE008BD02QPl&c=1423.r.
FEATURES
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 42.7%; Score 957.4; DB 5; Length 1097;
Best Local Similarity 93.7%; Pred. No. 5.6e-200;
Matches 959; Conservative 41; Mismatches 23; Indels 1; Gaps 1;
QY 1 CGTCACACACAGTACGTCCCTCGGTCTCAGTCGGCCGACGCCCTCTCAGTCCTCCCAACCC 60
Db 75 CGTCACACACAGTACGTCCCTCGGTCTCAGTCGGCCGACGCCCTCTCAGTCCTCCCAACCC 134
QY 61 CCACACCGCCCGCGGTCTCTGAGACGCGGCCCGCGCGCGCGCGCGAGCTGCAGCATC 120
Db 135 CCACACCGCCCGCGGTCTCTGAGACGCGGCCCGCGCGCGCGCGAGCTGCAGCATC 194
QY 121 ATCTCCACCTTCAGACCATGGAAGACCTGGACCAAGTCTCTCTGTTCTCTGCTCTCGGACA 180
Db 195 ATCTCCACCTTCAGACCATGGAAGACCTGGACCAAGTCTCTCTGTTCTCTGCTCTCGGACA 254
QY 181 GCCCACCCCGCCGACGCCCTTCAAGTACCAAGTCTCTGAGGAGAGCCCGAGGACGAGG 240
Db 255 GCCCACCCCGCCGACGCCCTTCAAGTACCAAGTCTCTGAGGAGAGCCCGAGGACGAGG 314
QY 241 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 315 AGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
QY 301 TGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 375 TGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434
QY 361 GCGCGCCCTTCATGACCTTCGGAATGACTTTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 435 GCGCGCCCTTCATGACCTTCGGAATGACTTTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 494
QY 421 CGGCCGCTCCCCCGCTCGCCCGGAGCGGAGCGGCTCTTGGGACCCGAGCCCGGTGTCTGT 480


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Db 495 CGGCGCTCCCGCGTCCCGCGAGGCGCGTCTTGGACCCGAGCCGGTGCCT 554
Qy 481 CGACCGTCCCGCGCCATCCCGCTGTCTGTGCGCAGTCTCGCCCTCCAAGCTCCCTG 540
Db 555 CGACCGTCCCGCGCCATCCCGCTGTCTGTGCGCAGTCTCGCCCTCCAAGCTCCCTG 614
Qy 541 AGACGAGCGAGCTCCCGCGCGCTCCCTCTCTCTCCCGCGCAGCGTGAAGCCCGCAGG 600
Db 615 AGACGAGCGAGCTCCCGCGCGCTCCCTCTCTCTCTCCCGCGCAGCGTGAAGCCCGCAGG 674
Qy 601 CAGAGCCGTGTGACCGCGCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 675 CAGAGCCGTGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 734
Qy 661 CGCCCAAGCGCAGCGGCTCCCTCGGCGCTCAGTGTGTGTGACCTCTCTGTCTGAGAGACA 720
Db 735 GGCCCAAGCGCAGCGGCTCCCTCGGCGCTCAGTGTGTGTGACCTCTCTGTCTGAGAGACA 794
Qy 721 TTAAGAAGACTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 795 TTAAGAAGACTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 854
Qy 781 TCACATTTGTGAGGTAAACGCTACATTTGCTGTGCGCGCTCTCTGTGACCATCAGCT 840
Db 855 TCACATTTGTGAGGTAAACGCTACATTTGCTGTGCGCGCTCTCTGTGACCATCAGCT 914
Qy 841 TTAGGATATACAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 900
Db 915 TTAGGATATACAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCA 974
Qy 901 GGGCATATCTGAATCTGAAGTGTCTATATCTGAGGAGTGTGTGTGAGAGTACAGTAAT 960
Db 975 GGGCATATCTGAATCTGAAGTGTCTATATCTGAGGAGTGTGTGTGAGAGTACAGTAAT 1034
Qy 961 CTGCTCTGTGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020
Db 1035 YTKCTCTTKGTCWAKTTGAATKSMGAAARGAA-HYARGSGCCYTTTTTTTWTATK 1093
Qy 1021 ATTT 1024
Db 1094 WTTT 1097
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RESULT 6

BX426504/c
LOCUS BX426504 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
DEFINITION clone CS0DH001YJ01 3-PRIME, mRNA sequence.

ACCESSION BX426504

VERSION BX426504.2 GI:47012045

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (bases 1 to 1028)

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30784554.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

into enriched, double-strand cDNA was digested with Not I and cloned

the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 1423.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0AH001CE01NP1&c=1423.r.

FEATURES
source

Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DH001YJ01"
/tissue="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 40.9%; Score 917.2; DB 5; Length 1028;
Best Local Similarity 97.3%; Pred. No. 4e-191;
Matches 987; Conservative 2; Mismatches 10; Indels 15; Gaps 5;
Qy 1199 TAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATGAAGCGCAAGCTGAATG 1258
Db 1011 TAAAGATGCTATGGCT-AAATCCAAAGCAAAATCCCTGGATGAAGCGCAAGCTGAATG 953
Qy 1259 AAAACGCCCAAAATATAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATTATAC 1318
Db 952 AAAACGCCCAAAATATAGTAGAGTTCATCTTTAAAGGGGATATTCATTTGATTATAC 893
Qy 1319 GGGGGAGGGTCAGGGAAGAACGAACTTGACGTTGACGTGCAGTTTCACAGATCGTTGTT 1378
Db 892 GGGGGAGGGTCAGGGAAGAACGAACTTGACGTTGACGTGCAGTTTCACAGATCGTTGTT 834
Qy 1379 AGATCTTTATTTTAGCCATGCACTGTTGTGAGGAAAAATACCTGCTTTGACTGCCATG 1438
Db 833 AGATCTTTATTTTAGCCATGCACTGTTGTGAGGAAAAATACCTGCTTTGACTGCCATG 774
Qy 1439 TGTTTCATCTTAAGTATTTAGTGTGCTGCTATGTATGGATTTAAACGTAATCATATCTT 1498
Db 773 TGTTTCATCTTAAGTATTTAGTGTGCTGCTATGTATGGATTTAAACGTAATCATATCTT 714
Qy 1499 TTTC---CTATCTGAGGCACCTGCGTAATAAAACCTGTATATTTTACTTTGTTGTCAG 1554
Db 713 TTTCCTATCTATCTGAGGCACCTGCGTAATAAAACCTGTATATTTTACTTTGTTGTCAG 654
Qy 1555 ATAGTCTTGGCCGATCTTGGCAAGTTGCAGAGATGTTGGAGCTAGAAAAA 1614
Db 653 ATAGTCTTGGCCGATCTTGGCAAGTTGCAGAGATGTTGGAGCTAG-----AAAAA 600
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Qy 1675 TGAATCTTTTGTAGACGAGATCATACCGTAAAGCAGCAATGACAAAGCTGCTTTTC 1734
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Qy 1735 TGCTATGTTCTAGTGTATTTGTCACCTTTTACTGTTATTAATTTGCAATATAAGTAAT 1794
Db 479 TGCTATGTTCTAGTGTATTTGTCACCTTTTACTGTTATTAATTTGCAATATAAGTAAT 420
Qy 1795 ATGATATATATATATAGTGTATTTTCAAAAGCTTAGACCTTTTACCTTCAGGCGACCCAC 1854
Db 419 ATGATATATATATATAGTGTATTTTCAAAAGCTTAGACCTTTTACCTTCAGGCGACCCAC 360
Qy 1855 AGTGTCTGATTTTCAGAGTCAGTTCATGTTGGTTATACATGTGTAGTTCCTCAAGCACAATAG 1914
Db 359 AGTGTCTGATTTTCAGAGTCAGTTCATGTTGGTTATACATGTGTAGTTCCTCAAGCACAATAG 300
Qy 1915 CTAGAAGCAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCACATGAATGCAACA 1974
Db 299 CTAGAAGCAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCACATGAATGCAACA 240
Qy 1975 CATAGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2034

[illegible]

[illegible]

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12120 row: m column: 14
 High quality sequence stop: 641.
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 /clone="IMAGE:5494837"
 /tissue_type="retinoblastoma"
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 /clone_lib="NIH_MGC_67"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.75 Kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match	37.7%	Score 844.6	DB 4	Length 1008	
Best Local Similarity	96.7%	Pred. No. 4e-175			
Matches 926	Conservative	0	Mismatches 25	Indels 7	Gaps 6
Qy	1219	TCCAAGCAGAAAAATCCCTGGAGTTCAAGCGGCAAAAGCTGAATGAAAAACGCCCAAAATAATTAG	1278		
Db	1	TCCACGCAAAATCCCTGGATTCGAGCGCAAGCTGAATGAAAAACGCCCAAAATNATTAG	60		
Qy	1279	TAGGAGTTCAATCTTTAAAGGGGATATTCATTTTGATTATACGGGGGAGGTCAGGGGAAGAA	1338		
Db	61	TAGGAGTTCACTTTTAAAGGGGATATTCATTTTGATTATACGGGGGAGGTCAGGGGAAGAA	120		
Qy	1339	CGAACCTTGAGCTGTCAGTGCAGTTCACAGATCGTTGTTTAGATCTTTATTTTATGCGCAT	1398		
Db	121	CGAACCTTGAGCTGTCAGTGCAGTTCACAGATCGTTGTTTAGATCTTTATTTTATGCGCAT	180		
Qy	1399	GCACCTGTTGAGGAAAAATTTACCTGCTCTTGAGCTGCCATGTTTCATCATCTTTAAAGTATT	1458		
Db	181	GCACCTGTTGAGGAAAAATTTACCTGCTCTTGAGCTGCCATGTTTCATCATCTTTAAAGTATT	240		
Qy	1459	GTAAGCTGCTATGTAATGGATTTTAAACCGTAATCATATCTTTTTCCTATCTGAGGCACTGG	1518		
Db	241	GTAAGCTGCTATGTAATGGATTTTAAACCGTAATCATATCTTTTTCCTATCTGAGGCACTGG	300		
Qy	1519	TGGAATAAAAAACCTGTATATTTTACTTTGTTCAGATAGTCTTTCGCGCATCTTGCGCAAG	1578		
Db	301	TGGAATAAAAAACCTGTATATTTTACTTTGTTCAGATAGTCTTTCGCGCATCTTGCGCAAG	360		
Qy	1579	TTGCAGAGATGGTGGAGCTAG-AAAAAAGGAGGCTTTTTCAGTTCGTGCACTG	1637		
Db	361	TTGCAGAGATGGTGGAGCTAGAAAAAAGGAGGCTTTTTCAGTTCGTGCACTG	420		
Qy	1638	TGTAATGTCGTGTAGATTGATGTCAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGAT	1697		
Db	421	TGTAATGTCGTGTAGATTGATGTCAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGAT	480		
Qy	1698	CATACCGGTAAAGCAGGAATGCAAAAGCTTGCCTTTTCTGGTATGTTCTAGGTGTATTGTG	1757		
Db	481	CATACCGGTAAAGCAGGAATGCAAAAGCTTGCCTTTTCTGGTATGTTCTAGGTGTATTGTG	540		
Qy	1758	ACTTTTACTGTTATA TTAAATGCGCAATATAAGTAAATATAGATATATATATATATATATGTAATGTT	1817		
Db	541	ACTTTTACTGTTATA TTAAATGCGCAATATAAGTAAATATAGATATATATATATATATATGTAATGTT	600		

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Qy 1818 TCACAAAGCTTAGACCTTTACCTTCAGCCACCCACAGCTGCTGTGATATTTTCAGAGTCAG 1877
Db 601 TCACAAAGCTTAGACCTTTACCTTCAGCCACCCACAGCTGCTGTGATATTTTCAGAGTCAG 660
Qy 1878 TCATTGGTTATACATGTGTAGTTCACAAAGCACATAGCTAGAGCAAGAAATATTTCTAGG 1937
Db 661 TCATTGGTTATACATGTGTAGTTCACAAAGCACATAGCTAGAGCAAG- AATATTTCTAGG 719
Qy 1938 AGCACTACCAATCTCTTTTCAACATGAATGCCACACATAGAACTCCAAACACATCAAT 1997
Db 720 AGCACTACCAATCTCTTTTCAACATGAATGCCACACATAGAACTCCNAC-ACATCAAT 777
Qy 1998 TTCAATTCACAGACTGACTGTAGTAAATTTTGTGCAGAACTCTATGACTGAATCTAATG 2057
Db 778 TTCAATTCACAGACTGACTGTAGTAAATTTTGTGCAGAACTCTATGAGGACTGAATCTAATG 837
Qy 2058 CTTCCAAAATGTTGTTTGTGCAAAATATCAAAATGTTTATGCAAGAAATATTTAA-T 2116
Db 838 CTTCCAAAATGTTGTTTGTGCAAAATATCAAAATGTTTATGCGCAGAAAATTTTAAAT 897
Qy 2117 TACAAAATGAAGATTTATACCAATG--TGTTTAAAGCTGTACTGAACTAAATCTGTGG 2172
Db 898 TCCAAAATTGAGATTTTATCCCTTGGTGGGTTTAAAGCTGTACTGGAACCTAAATCCTGG 955

RESULT 11
CK231727 1003 bp mRNA linear EST 09-DEC-2003
LOCUS ILLUMIGEN MQ 2869 Katze.MMBR Macaca mulatta cDNA 5' similar to
DEFINITION human RTM4 (Hs.436349), mRNA sequence.
ACCESSION CK231727
VERSION CK231727.1 GI:39638085
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2003.11.24. 765 Q20 bases. Assembles in contig w/ 2
member(s). Contig contains 1 (1.5%) lib members.
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 1003 Std Error: 0.00
Plate: CL000026 row: D column: 03
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POLYA-No.

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                        /sex="female"
                        /dev_stage="adult"
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                        /clone_lib="Katze MMBR"
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                        Cloning Kit (catalog #200450)"

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ORIGIN

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Query Match          37.7%; Score 844.2; DB 7; Length 1003;
Best Local Similarity 95.6%; Pred. No. 4.9e-175;
Matches 926; Conservative 0; Mismatches 28; Indels 15; Gaps 5;

Qy 858 GTGATCCAAGCTATCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT 917
Db 9 GAGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCT 68
Qy 918 GAAGTTGCTATATCTGAGGAGTTGGTTCAGAACTACAGTAATTTCTGCTCTTGGTCATGTG 977
Db 69 GAAGTTGCGATATCTGAGGAGTTGGTTTCAAGACTACAGTAATTTCTGCTCTTGGTCATGTG 128
Qy 978 AACTGCACGATTAAGAACTCAGCGCCCTCTTCTTAGTTCATGATTTAGTTAGTTCTCTG 1037
Db 129 AACTGCACGATTAAGAACTCAGCGCCCTCTTCTTAGTTCATGATTTAGTTAGTTCTCTG 188
Qy 1038 AAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTCCCTTGTTTAATGTTGCTGACA 1097
Db 189 AAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTCCCTTGTTTAATGTTGCTGACG 248
Qy 1098 CTACTGATTTGGCTCTCAATTTCACTCTTCACTGTTTCTGTTATTTAATGAACCGCATCAG 1157
Db 249 CTACTGATTTGGCTCTCAATTTCACTCTTCACTGTTTCTGTTATTTAATGAACCGCATCAG 308
Qy 1158 GCACAGATAGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAGATGCTATGGCTAAA 1217
Db 309 GCACAGATAGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAGATGCTATGGCTAAA 368
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Db 369 ATCCAAGCAAAAATCCCTGGATTTGAAGCGCAAGCTGAATGAAAGCCCAAAATAATTA 428
Qy 1278 GTAGGAGTTTCATCTTTAAAGGGGATATTCATTTGATATATACGGGGAGGGTTCAGGGGAAGA 1337
Db 429 CTAGGAGTTTCATCTTTAAAGGGGATATTCATTTGATATATGCGGGAGGCTCAGGGAAGA 488
Qy 1338 ACGAACCCTTGACGTTGCGAGTGCGATTTTCACAGATCGTGTGTAGATCTTTATTTTAGCCA 1397
Db 489 ACGAACCCTTGACATTTGCGAGTGCGATTTTCACAGATCGTGTGTAGATCTTTATTTTAGCCA 548
Qy 1398 TGCACCTGTTGTGAGGAAAATTAACCTGCTGTGCTGACATGCTTCATCATCTTTAAGTAT 1457
Db 549 TGCACCTGTTGTGAGGAAAATTAACCTGCTGTGCTGACATGCTTCATCATCTTTAAGTAT 607
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Db 668 GTGGAATAAAAAACCTGTATATTTTACTTTTGTGCGAGTATGCTTGTGCAATCTTTGGCAA 727
Qy 1578 GTTGCAGAGATGCTGGAGCTAGAAAAAAGGAGCCCTTTTCAGTTTGTGCACTG 1637
Db 728 GTTGCAGAGATGCTGGAGTTAG-----AAAAAAGGAGCCCTTTTCAGTTTGTGCACTG 779
Qy 1638 TGTATGCTCGCTGTAGATTTGATGCGAATTTCTGAAATGAAATGTTTGTGTTAGACGAGAT 1697
Db 780 TGTATGCTCGCTGTAGATTTGATGCGAATTTCTGAAATGAAATGAAA-----TGTGTTAGACGAGAT 835
Qy 1698 CATACCGGTAAGCAGGAATGACAAAAGCTGCTTTTCTGTTATGTTCTAGGTGTTATGTTG 1757
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Db 896 AATTTTACTGTTTATATTAATTTGCCCAATATAGTAAATTAATAATATATATATATATAGTG 955
Qy 1816 TTTTCACAAA 1824
Db 956 GTTTCCCAA 964

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Query Match		37.1%; Score 831; DB 7; Length 956;
Best Local Similarity		95.3%; Pred. No. 4e-172;
Matches 914; Conservative		0; Mismatches 30; Indels 15; Gaps 5;
QY	885	GAAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGAGTTGGTT 944
DB	1	GAAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCGATATCTGAGGAGTTGGTT 60
QY	945	CAGAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGCAGATACAGATAAGGAACTCAGGGCC 1004
DB	61	CAGAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGCAGATACAGATAAGGAACTCAGGGCC 120
QY	1005	CTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGAGTGTGATGTTGGGTATTT 1064
DB	121	CTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGAGTGTGATGTTGGGTATTT 180
QY	1065	ACCTATGTTGGTCTGTTTAAATGCTGTGACATCTACTGATTTTGGCTCTCATTTCACTC 1124
DB	181	ACCTATGTTGGTCTGTTTAAATGCTGTGACCTACTGATTTTGGCTCTCATTTCACTC 240
QY	1125	TTCAGTGTCTCTGTTTAAATGCTGTGACGATCAGGCACAGATAGATCATTTCTAGGACTT 1184
DB	241	TTCAGTGTCTCTGTTTAAATGCTGTGACGATCAGGCACAGATAGATCATTTCTAGGACTT 300
QY	1185	GCAATAAGAAATGTTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATCCCTGGATTGAAG 1244
DB	301	GCAATAAGAAATGTTTAAAGATGCTATGGCTTAAATCCAAAGCGAAATCCCTGGATTGAAG 360
QY	1245	CGCAAGCTGAATGAAACGCCCAAAATAATAGTAGGAGTTTCATCTTTAAAGGGGATAT 1304
DB	361	CGCAAGCTGAATGAAACGCCCAAAATAATAGTAGGAGTTTCATCTTTAAAGGGGGTAT 420
QY	1305	TCATTTGATTTACGGGGAGGCTCAGGAGAAAGCAACCTTGAGTTGCGATGCGAGTTT 1364
DB	421	TCATTTGATTTACGGGGAGGCTCAGGAGAAAGCAACCTTGACATTCGAGTGCAGTTT 480
QY	1365	CACAGATCGTTTGTAGATCTTTATTTTATGAGCATGCACTGTTGTGAGGAAAAATTTACCTG 1424
DB	481	CACAGATCGTTTGTAGATCTTTATTTTATGAGCATGCACTGTTGTGAGGAAAAATTTACCTG 540
QY	1425	TCTTGACGCCATGTTGTTTCATCATCTTAAAGTATTTGTAAGCTGCTATGTATGATTTAAAC 1484
DB	541	TCTTGACGCCATGTTGTTTCATCATC- TAAGTATTTGTAAGCTGCTATGTATGATTTAAAC 599
QY	1485	CGTAATCATATCTTTTCTCTATCTGAGGCACTGTGGAAATAAAACCTGTATATTTTAC 1544
DB	600	CGTAATCATATCTTTTCTCTATCTGAGGCACTGTGGAAATAAAACCTGTATATTTTAC 659
QY	1545	TTTGTTCAGATAGTCTTTGCGCATCTTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAA 1604
DB	660	TTTGTTCAGGTTAGTCTTTGCTGATCTTTGGCAAGTTGCAGAGATGGTGGAGTTAG- ---- 714
QY	1605	AAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGCTCGGTGATGATGATGACGA 1664
DB	715	--- AAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGCTCGGTGATGATGATGACGA 771
QY	1665	TTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAG 1724
DB	772	TTTTCTGAAATGAAATGTTTGTGTTAGACGAAATCATACCGGTAAAGCAGGAATGAAAT 827
QY	1725	CTTGTCTTCTGGTATGTTTCTAGGTGTATTTGTGAC- TTTTACTGTATATTAATTTGCCAA 1783
DB	828	CTTGTCTTCTGGTATGTTTCTAGGTGTATTTGTGACTTTTACTGTATATTAATTTGCCAA 887
QY	1784	TATAAGTAAATATAGATATATATGATATA- GTGTTTCAAAAGCTTAGACCTTTACCTT 1841
DB	888	TATAAGTAAATATAGATTTAAATATATATAGGTGTTTCAAAAGCTTTAAACCTTTACCT 946
RESULT 15		
CN647521		1031 bp mRNA linear EST 13-MAY-2004
LOCUS		

DEFINITION		ILLUMIGEN_MCO_28658 Katze_MMR Macaca mulatta cDNA clone IBIUM:7529
		5' similar to Bases 129 to 1018 highly similar to human RTN4
		(Hs.436349), mRNA sequence.
ACCESSION		CN647521
VERSION		CN647521.1 GI:47160964
KEYWORDS		EST.
SOURCE		Macaca mulatta (rhesus monkey)
ORGANISM		Macaca mulatta
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
		Cercopitheciinae; Macaca.
REFERENCE		1 (bases 1 to 1031)
AUTHORS		Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE		Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL		Unpublished (2003)
COMMENT		Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagness@illumigen.com Sequenced on 2004.03.24. 773 Q20 bases. PCR Primers FORWARD: CCCTCACTAAAGGGAACAAAA BACKWARD: CACTATAGGCGGAATTTGGGTA Insert Length: 1031 Std Error: 0.00 Plate: CL000187 row: G column: 05 Seq primer: CCCTCACTAAAGGGAACAAAA POLY-A-No.
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		/db_xref="taxon:9544"
		/clone="IBIUM:7529"
		/sex="Female"
		/dev_stage="adult"
		/lab_host="E. coli SOLR"
		/note="Organ: brain; Vector: Uni-ZAP XR; Site:1; EcoR I;"
		Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
		kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
		Cloning Kit (Catalog #200450)"
ORIGIN		
Query Match		36.6%; Score 819.2; DB 7; Length 1031;
Best Local Similarity		95.6%; Pred. No. 1.6e-169;
Matches 864; Conservative		0; Mismatches 38; Indels 2; Gaps 2;
QY	692	GGTTGTTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 751
DB	128	GGTTGTTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAG 187
QY	752	CCTATTCTGCTGCTTCATTTGACAGTATTCAGCATTTGAGCGTAAACGCTCACTTGC 811
DB	188	CCTATTCTGCTGCTTCATTTGACAGTATTCAGCATTTGAGCGTAAACGCTCACTTGC 247
QY	812	CTTGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTAT 871
DB	248	CTTGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTAT 307
QY	872	CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 931
DB	308	CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATC 367
QY	932	TGAGAGTTGGTTCAGAAAGTACAGTAATCTTGCTCTTGCTCATGTGAACTGCACGATAAA 991
DB	368	TGAGAGTTGGTTCAGAAAGTACAGTAATCTTGCTCTTGCTCATGTGAACTGCACGATAAA 427
QY	992	GGAACTCAGGGCCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAAGTTTGCACTGTT 1051
DB	428	GGAACTCAGGGCCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAAGTTTGCACTGTT 487

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